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APPLICATION NUMBER: 10/778,908

FILING DATE: February 13, 2004

RELATED PCT APPLICATION NUMBER: PCT/US05/04714



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17157 U.S. PTO
021304

Attorney's Docket No. **1119-10**

PATENT

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021304

NONPROVISIONAL PATENT APPLICATION TRANSMITTAL

Sir:

Transmitted herewith for filing is the patent application of:

First Named Inventor (or Inventors):

**Dr. Thomas Tuschl
Dr. Markus Landthaler
Dr. Gunter Meister
Dr. Sebastien Pfeffer**

Title of Application:

ANTI-MICRORNA OLIGONUCLEOTIDE MOLECULES

1. Type of Application (37 C.F.R. 1.53(b))

This application is a(n):

☒ Original (nonprovisional) application.

☐ Continuing application:

☐ Divisional

☐ Continuation

☐ Continuation-in-Part (CIP)

of Serial No. _____, filed on _____.

CERTIFICATION UNDER 37 C.F.R. 1.10

I hereby certify that this New Application Transmittal and the documents referred to as enclosed herein are being deposited with the United States Postal Service on this date, **February 13, 2004**, in an envelope as "Express Mail to Addressee" Mailing Label Number **EL 747202340 US**, addressed to Mail Stop: Patent Application, Commissioner of Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Edna I. Gergel

Name of person mailing paper


Signature of person mailing paper

2. Benefit of Prior U.S. Application(s) (35 U.S.C. 119(e), 120, or 121)

- ☐ This new application claims the benefit of prior U.S. application(s).
- ☐ A Preliminary Amendment is enclosed amending this application to state the relation of this application to prior applications.
- ☐ The relation of this application to prior applications is stated in the application.

3. 35 U.S.C. 119(a)-(d) or 35 U.S.C. 365(a)-(b) Foreign Priority Claim for Prior Application

This application, and prior U.S. application(s), including any prior International Application designating the U.S., identified above in item 2, claim(s) priority from one or more foreign applications as follows:

(Country)	(Application No.)	(Filing Date) (mm/dd/yyyy)

- ☐ Please amend the specification by inserting, after the title, the following:
- ☐ "The application claims priority from Application No. _____ filed on _____."

Certified copy(ies) of the application(s) from which priority under 35 U.S.C. 119 is claimed:

- ☐ has(have) been filed on _____, in prior application _____, which was filed on _____.
- ☐ is (are) enclosed.
- ☐ will follow.

4. Enclosed Papers Required to Obtain Application Filing Date under 37 C.F.R. 1.53(b)

29 Pages of Specification
6 Pages of Claims
0 Pages of Abstract
3 Sheets of Drawings ☒ Formal ☐ Informal

5. Oath or Declaration

- ☐ Newly executed Oath or Declaration (original or copy) is enclosed.
- ☐ Copy of Oath or Declaration from prior continuation or divisional application _____ (37 C.F.R. 1.63(d)).
- ☐ The entire disclosure of the prior application, from which a copy of the oath or Declaration is supplied, is considered as being a part of the disclosure of the accompanying application and is hereby incorporated by reference therein.
- ☐ A Power of Attorney is included in the Oath or Declaration.
- ☒ Not enclosed.

6. Additional Papers Enclosed

- ☒ Return Receipt Postcard (specifically itemized) (M.P.E.P. § 503).
- ☐ Application Data Sheet (Voluntary under 37 C.F.R. 1.76).
- ☐ Preliminary Amendment.
- ☐ Information Disclosure Statement (37 C.F.R. 1.98).
- ☐ Form PTO-1449 ☐ Copies of IDS Citations
- ☐ Nucleotide and/or Amino Acid Sequence Listing computer-readable copy, paper copy, and statement verifying identity of computer-readable and paper copies.
- ☐ Certified Copy of Priority Document(s).
- ☐ Verified translation of non-English language application (37 C.F.R. 1.52(d)).
- ☐ Other: _____.

7. Assignment

- ☒ An assignment of the invention to ____.
- ☐ is enclosed. A separate:
- ☐ "Cover Sheet for Assignment (Document) Accompanying New Patent Application" is enclosed.
- ☐ Form PTO-1595 is enclosed.
- ☐ was made in prior application No. ____, filed on ____.
- ☐ A copy of the assignment (and any recordation cover sheet) is enclosed.
- ☐ will follow.
- ☒ Not enclosed.

8. Request That Application Not Be Published Pursuant to 35 U.S.C. 122(b)(2)

- ☐ Pursuant to 35 U.S.C. 122(b)(2), Applicant(s) hereby requests that this patent application not be published pursuant to 35 U.S.C. 122(b)(1). Applicant hereby certifies that the invention disclosed in this application has not and will not be the subject of an application filed in another country, or under a multilateral international agreement, that requires publication of applications 18 months after filing of the application.

Warning

An applicant who makes a request not to publish, but who subsequently files in a foreign country or under a multilateral international agreement specified in 35 U.S.C. 122(b)(2)(B)(i), must notify the Director of such filing not later than 45 days after the date of the filing of such foreign or international application. A failure of the applicant to provide such notice within the prescribed period shall result in the application being regarded as abandoned, unless it is shown to the satisfaction of the Director that the delay in submitting the notice was unintentional.

9. Fee Calculation (37 C.F.R. 1.16)

Utility Application (37 C.F.R. 1.16(a))

Basic Fee \$770.00

FEES FOR CLAIMS AS FILED					
Number filed	Number extra		Rate		
Total Claims (37 C.F.R. 1.16 (c))	47	- 20	= 27	x \$ 18.00	= \$ 486.00
Independent Claims (37 C.F.R. 1.16(b))	4	- 3	= 1	x \$ 86.00	= \$ 86.00
Multiple Dependent Claims (37 C.F.R. 1.16(d))			+ \$ 290.00	=	\$ 0.00
Fee Calculation for Extra Claims					\$ 572.00

☐ Amendment canceling extra claims enclosed.☐ Amendment deleting multiple-dependencies enclosed.Total Filing Fee Calculation **\$ 1,342.00****10. Small Entity Statement**☒ Small entity status is claimed under 37 C.F.R. 1.27.Filing Fee Calculation (50% of Filing Fee calculated in Item 9 above) **\$ 671.00****11. Fee Payment**☒ Not enclosed. No filing fee is to be paid at this time.☐ Enclosed:☐ Basic filing fee (Item 9 or 10 above) \$ _____☐ Fee for recording Assignment
\$40.00 (37 C.F.R. 1.21(h)) \$ _____☐ Processing and retention fee
\$130.00 (37 C.F.R. 1.53(d) and 1.21(l)) \$ _____Total fees enclosed **\$ 0.00.**

12. Method of Payment of Fees

- ☐ Check in the amount of \$_____.
- ☐ Charge Deposit Account No. _____ in the amount of \$_____.
A duplicate of this transmittal is enclosed.

13. Authorization to Charge Additional Fees

- ☐ The Commissioner is hereby authorized to charge the following additional fees by this paper and during the entire pendency of this application to Deposit Account No. _____:
- ☐ 37 C.F.R. 1.16(a), (f), or (g) (filing fees)
- ☐ 37 C.F.R. 1.16(b), (c), and (d) (presentation of extra claims)
- ☐ 37 C.F.R. 1.16(e) (surcharge for filing the basic fee and/or declaration at a date later than the filing date of the application)
- ☐ 37 C.F.R. 1.17 (application processing fees)

A duplicate of this transmittal is enclosed.

14. Instructions as to Overpayment

- ☒ Credit Deposit Account **08-2461**. ☐ Refund.

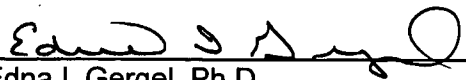
15. Correspondence Address

- ☒ Customer Number or Bar Code Label: **23869**

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Anti-MicroRNA Oligonucleotide Molecules

The invention claimed herein was made with the help of grant number 1 R01 GM068476-01 from NIH/NIGMS. The U.S. government has certain rights in the invention.

BACKGROUND OF THE INVENTION

RNA silencing is a fundamental mechanism of gene regulation that uses double-stranded RNA (dsRNA) derived 21- to 28-nucleotide (nt) small RNAs to guide mRNA degradation, control mRNA translation or chromatin modification. Recently, several hundred novel genes were identified in plants and animals that encode transcripts that contain short dsRNA hairpins.

Defined 22-nt RNAs, referred to as microRNAs (miRNAs), are reported to be excised by dsRNA specific endonucleases from the hairpin precursors. The miRNAs are incorporated into ribonucleoprotein particles (miRNPs).

Plant miRNAs target mRNAs containing sequence segments with high complementarity for degradation or suppress translation of partially complementary mRNAs. Animal miRNAs appear to act predominantly as translational repressors. However, animal miRNAs have also been reported to guide RNA degradation. This indicates that animal miRNPs act like small interfering RNA (siRNA)-induced silencing complexes (RISCs).

Understanding the biological function of miRNAs requires knowledge of their mRNA targets. Bioinformatic approaches have been used to predict mRNA targets, among which transcription factors and proapoptotic genes were prominent candidates. Processes such as *Notch* signaling, cell proliferation, morphogenesis and axon guidance appear to be controlled by miRNA genes.

Therefore, there is a need for materials and methods that can help elucidate the function of known and future microRNAs. Due to the ability of microRNAs to induce RNA degradation or repress translation of mRNA which encode important proteins, there is also a need for novel compositions for inhibiting microRNA-induced cleavage or repression of mRNAs.

SUMMARY THE INVENTION

In one embodiment, the invention provides an isolated single stranded anti-microRNA molecule comprising a minimum of ten moieties and a maximum of fifty moieties on a molecular backbone, the molecular backbone comprising backbone units, each moiety comprising a base bonded to a backbone unit, each base forming a Watson-Crick base pair with a complementary base wherein at least ten contiguous bases have the same sequence as a sequence of bases in any one of the anti-microRNA molecules shown in Tables 1-4, except that up to thirty percent of the bases pairs may be wobble base pairs, and up to 10% of the contiguous bases are additions, deletions, mismatches, or combinations thereof; no more than fifty percent of the contiguous moieties contain deoxyribonucleotide backbone units; the moiety in the molecule at the position corresponding to position 11 of the microRNA is non-complementary; and the molecule is capable of inhibiting microRNP activity.

In another embodiment, the invention provides a method for inhibiting microRNP activity in a cell, the microRNP comprising a microRNA molecule, the microRNA molecule comprising a sequences of bases complementary of the sequence of bases in a single stranded anti-microRNA molecule, the method comprising introducing into the cell the single-stranded anti-microRNA molecule comprising a sequence of a minimum of ten moieties and a maximum of fifty moieties on a molecular backbone, the molecular backbone comprising backbone units, each moiety comprising a base bonded to a backbone unit, each base forming a Watson-Crick base pair with a complementary base, wherein at least ten contiguous bases of the anti-microRNA molecule are complementary to the microRNA, except that up to thirty percent of the bases may be substituted by wobble base pairs, and up to ten percent of the at least ten moieties are addition, deletions, mismatches, or combinations thereof; no more than fifty percent of the contiguous moieties contain deoxyribonucleotide backbone units; and the moiety in the molecule at the position corresponding to position 11 of the microRNA is non-complementary.

In another embodiment, the invention provides an isolated microRNA molecule comprising a minimum of ten moieties and a maximum of fifty moieties on a molecular backbone, the molecular backbone comprising backbone units, each moiety comprising a base bonded to a backbone unit, wherein at least ten contiguous bases have the same sequence as a

sequence of bases in any one of the microRNA molecules shown in Table 2, except that up to thirty percent of the bases pairs may be wobble base pairs, and up to 10% of the contiguous bases are additions, deletions, mismatches, or combinations thereof; and no more than fifty percent of the contiguous moieties contain deoxyribonucleotide backbone units.

In another embodiment, the invention provides an isolated microRNA molecule comprising a minimum of ten moieties and a maximum of fifty moieties on a molecular backbone, the molecular backbone comprising backbone units, each moiety comprising a base bonded to a backbone unit, wherein at least ten contiguous bases have any one of the microRNA sequences shown in Tables 1, 3 and 4, except that up to thirty percent of the bases pairs may be wobble base pairs, and up to 10% of the contiguous bases are additions, deletions, mismatches, or combinations thereof; no more than fifty percent of the contiguous moieties contain deoxyribonucleotide backbone units; and is modified for increased nuclease resistance.

DESCRIPTION OF THE FIGURES

Figure 1 shows the modified nucleotide units discussed in the specification. B denotes any one of the following nucleic acid bases: adenosine, cytidine, guanosine, thymine, or uridine.

Figure 2. Antisense 2'-O-methyl oligoribonucleotide specifically inhibit miR-21 guided cleavage activity in HeLa cell S100 cytoplasmic extracts. The black bar to the left of the RNase T1 ladder represents the region of the target RNA complementary to miR-21. Oligonucleotides complementary to miR-21 were pre-incubated in S100 extracts prior to the addition of ³²P-cap-labelled cleavage substrate. Cleavage bands and T1 hydrolysis bands appear as doublets after a 1-nt slipping of the T7 RNA polymerase near the middle of the transcript indicated by the asterisk.

Figure 3. Antisense 2'-O-methyl oligoribonucleotides interfere with endogenous miR-21 RNP cleavage in HeLa cells. HeLa cells were transfected with pHcRed and pEGFP or its derivatives, with or without inhibitory or control oligonucleotides. EGFP and HcRed protein fluorescence were excited and recorded individually by fluorescence microscopy 24 h after transfection. Co-expression of co-transfected reporter plasmids was documented by superimposing of the fluorescence images in the right panel.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to an isolated single stranded anti-microRNA molecule. The molecule comprises a minimum number of ten moieties, preferably a minimum of thirteen, more preferably a minimum of fifteen, even more preferably a minimum of 18, and most preferably a minimum of 21 moieties.

The anti-microRNA molecule comprises a maximum number of fifty moieties, preferably a maximum of forty, more preferably a maximum of thirty, even more preferably a maximum of twenty-five, and most preferably a maximum of twenty-three moieties. A suitable range of minimum and maximum number of moieties may be obtained by combining any of the above minima with any of the above maxima.

Each moiety comprises a base bonded to a backbone unit. In this specification, a base refers to any one of the nucleic acid bases present in DNA or RNA. The base can be a purine or pyrimidine. Examples of purine bases include adenine (A) and guanine (G). Examples of pyrimidine bases include thymine (T), cytosine (C) and uracil (U). Each base of the moiety forms a Watson-Crick base pair with a complementary base.

Watson-Crick base pairs as used herein refers to the hydrogen bonding interaction between, for example, the following bases: adenine and thymine (A = T); adenine and uracil (A = U); and cytosine and guanine (C = G). The adenine can be replaced with 2,6-diaminopurine without compromising base-pairing.

The backbone unit may be any molecular unit that is able stably to bind to a base and to form an oligomeric chain. Suitable backbone units are well known to those in the art.

For example, suitable backbone units include sugar-phosphate groups, such as the sugar-phosphate groups present in ribonucleotides, deoxyribonucleotides, phosphorothioate deoxyribose groups, N'3-N'5 phosphoroamidate deoxyribose groups, 2'O-alkyl-ribose phosphate groups, 2'-O-alkyl-alkoxy ribose phosphate groups, ribose phosphate group containing a methylene bridge, 2'-Fluororibose phosphate groups, morpholino phosphoroamidate groups, cyclohexene groups, tricyclo phosphate groups, and amino acid molecules.

In one embodiment, the anti-microRNA molecule comprises at least one moiety which is a ribonucleotide moiety or a deoxyribonucleotide moiety.

In another embodiment, the anti-microRNA molecule comprises at least one moiety which confers increased nuclease resistance. The nuclease can be an exonuclease, an endonuclease, or both. The exonuclease can be a 3'→5' exonuclease or a 5'→3' exonuclease. Examples of 3'→5' human exonuclease include PNPT1, Werner syndrome helicase, RRP40, RRP41, RRP42, RRP45, and RRP46. Examples of 5'→3' exonuclease include XRN2, and FEN1. Examples of endonucleases include Dicer, Drosha, RNase4, Ribonuclease P, Ribonuclease H1, DHP1, ERCC-1 and OGG1. Examples of nucleases which function as both an exonuclease and an endonuclease include APE1 and EXO1.

An anti-microRNA molecule comprising at least one moiety which confers increased nuclease resistance means a sequence of moieties wherein at least one moiety is not recognized by a nuclease. Therefore, the nuclease resistance of the molecule is increased compared to a sequence containing only unmodified ribonucleotide, unmodified deoxyribonucleotide or both. Such modified moieties are well known in the art, and were reviewed, for example, by Kurreck, *Eur. J. Biochem.* 270, 1628-1644 (2003).

A modified moiety can occur at any position in the anti-microRNA molecule. For example, to protect the anti-microRNA molecule against 3'→5' exonucleases, the molecule can have at least one modified moiety at the 3' end of the molecule and preferably at least two modified moieties at the 3' end. If it is desirable to protect the molecule against 5'→3' exonuclease, the anti-microRNA molecule can have at least one modified moiety and preferably at least two modified moieties at the 5' end of the molecule. The anti-microRNA molecule can also have at least one and preferably at least two modified moieties between the 5' and 3' end of the molecule to increase resistance of the molecule to endonucleases. In one embodiment, all of the moieties are nuclease resistant.

In another embodiment, the anti-microRNA molecule comprises at least one modified deoxyribonucleotide moiety. Suitable modified deoxyribonucleotide moieties are known in the art.

A suitable example of a modified deoxyribonucleotide moiety is a phosphorothioate deoxyribonucleotide moiety. See structure 1 in figure 1. An anti-microRNA molecule comprising more than one phosphorothioate deoxyribonucleotide moiety is referred to as phosphorothioate (PS) DNA. See, for example, Eckstein, *Antisense Nucleic Acids Drug Dev.* 10, 117-121 (2000).

Another suitable example of a modified deoxyribonucleotide moiety is an N³-N⁵ phosphoroamidate deoxyribonucleotide moiety. See structure 2 in figure 1. An oligonucleotide molecule comprising more than one phosphoroamidate deoxyribonucleotide moiety is referred to as phosphoroamidate (NP) DNA. See, for example, Gryaznov *et al.*, *J. Am. Chem. Soc.* 116, 3143-3144 (1994).

In another embodiment, the molecule comprises at least one modified ribonucleotide moiety. Suitable modified ribonucleotide moieties are known in the art.

A suitable example of a modified ribonucleotide moiety is a ribonucleotide moiety that is substituted at the 2' position. The substituents at the 2' position may, for example, be a C₁ to C₄ alkyl group. The C₁ to C₄ alkyl group may be saturated or unsaturated, and unbranched or branched. Some examples of C₁ to C₄ alkyl groups include ethyl, isopropyl, and allyl. The preferred C₁ to C₄ alkyl group is methyl. See structure 3 in figure 1. An oligoribonucleotide molecule comprising more than one ribonucleotide moiety that is substituted at the 2' position with a C₁ to C₄ alkyl group is referred to as a 2'-O-(C₁-C₄ alkyl) RNA, e.g., 2'-O-methyl RNA (OMe RNA).

Another suitable example of a substituent at the 2' position of a modified ribonucleotide moiety is a C₁ to C₄ alkoxy - C₁ to C₄ alkyl group. The C₁ to C₄ alkoxy (alkyloxy) and C₁ to C₄ alkyl group may comprise any of the alkyl groups described above. The preferred C₁ to C₄ alkoxy - C₁ to C₄ alkyl group is methoxyethyl. See structure 4 in figure 1. An oligonucleotide molecule comprising more than one ribonucleotide moiety that is substituted at the 2' position with a C₁ to C₄ alkoxy-C₁ to C₄ alkyl group is referred to as a 2'-O-(C₁ to C₄ alkoxy - C₁ to C₄ alkyl) RNA, e.g., 2'-O-methoxyethyl RNA (MOE RNA).

Another suitable example of a modified ribonucleotide moiety is a ribonucleotide that has a methylene bridge between the 2'-oxygen atom and the 4'-carbon atom. See structure 5 in figure 1. An oligoribonucleotide molecule comprising more than one ribonucleotide moiety that has a methylene bridge between the 2'-oxygen atom and the 4'-carbon atom is referred to as locked nucleic acid (LNA). See, for example, Kurreck *et al.*, *Nucleic Acids Res.* *30*, 1911-1918 (2002); Elayadi *et al.*, *Curr. Opin. Invest. Drugs* *2*, 558-561 (2001); Ørum *et al.*, *Curr. Opin. Mol. Ther.* *3*, 239-243 (2001); Koshkin *et al.*, *Tetrahedron* *54*, 3607-3630 (1998); Obika *et al.*, *Tetrahedron Lett.* *39*, 5401-5404 (1998). Locked nucleic acids are commercially available from Proligo (Paris, France and Boulder, Colorado, USA).

Another suitable example of a modified ribonucleotide moiety is a ribonucleotide that is substituted at the 2' position with fluoro group. A modified ribonucleotide moiety having a fluoro group at the 2' position is a 2'-fluororibonucleotide moiety. Such moieties are known in the art. Molecules comprising more than one 2'-fluororibonucleotide moiety are referred to herein as 2'-fluororibo nucleic acids (FANA). See structure 7 in figure 1. Damha *et al.*, *J. Am. Chem. Soc.* *120*, 12976-12977 (1998).

In another embodiment, the anti-microRNA molecule comprises at least one base bonded to an amino acid residue. Moieties that have at least one base bonded to an amino acid residue will be referred to herein as peptide nucleic acid (PNA) moieties. Such moieties are nuclease resistance, and are known in the art. Molecules having more than one PNA moiety are referred to as peptide nucleic acids. See structure 6 in figure 1. Nielson, *Methods Enzymol.* *313*, 156-164 (1999); Elayadi, *et al. id.*; Braasch *et al.*, *Biochemistry* *41*, 4503-4509 (2002), Nielsen *et al.*, *Science* *254*, 1497-1500 (1991).

The amino acids can be any amino acid, including natural or non-natural amino acids. Naturally occurring amino acids include, for example, the twenty most common amino acids normally found in proteins, i.e., alanine (Ala), arginine (Arg), asparagine (Asn), aspartic acid (Asp), cysteine (Cys), glutamine (Glu), glutamic acid (Glu), glycine (Gly), histidine (His), isoleucine (Ileu), leucine (Leu), lysine (Lys), methionine (Met), phenylalanine (Phe), proline (Pro), serine (Ser), threonine (Thr), tryptophan, (Trp), tyrosine (Tyr), and valine (Val).

The non-natural amino acids may, for example, comprise alkyl, aryl, or alkylaryl groups. Some examples of alkyl amino acids include α -aminobutyric acid, β -aminobutyric acid, γ -aminobutyric acid, δ -aminovaleric acid, and ϵ -aminocaproic acid. Some examples of aryl amino acids include ortho-, meta, and para-aminobenzoic acid. Some examples of alkylaryl amino acids include ortho-, meta-, and para-aminophenylacetic acid, and γ -phenyl- β -aminobutyric acid.

Non-naturally occurring amino acids also include derivatives of naturally occurring amino acids. The derivative of a naturally occurring amino acid may, for example, include the addition or one or more chemical groups to the naturally occurring amino acid.

For example, one or more chemical groups can be added to one or more of the 2', 3', 4', 5', or 6' position of the aromatic ring of a phenylalanine or tyrosine residue, or the 4', 5', 6', or 7' position of the benzo ring of a tryptophan residue. The group can be any chemical group that can be added to an aromatic ring. Some examples of such groups include hydroxyl, C₁-C₄ alkoxy, amino, methylamino, dimethylamino, nitro, halo (i.e., fluoro, chloro, bromo, or iodo), or branched or unbranched C₁-C₄ alkyl, such as methyl, ethyl, n-propyl, isopropyl, butyl, isobutyl, or t-butyl.

Furthermore, other examples of non-naturally occurring amino acids which are derivatives of naturally occurring amino acids include norvaline (Nva), norleucine (Nle), and hydroxyproline (Hyp).

The amino acids can be identical or different from one another. Bases are attached to the amino acid unit by molecular linkages. Examples of linkages are methylene carbonyl, ethylene carbonyl and ethyl linkages. (Nielsen et al., *Peptide Nucleic Acids-Protocols and Applications*, Horizon Scientific Press, pages 1-19; Nielsen et al., *Science* 254: 1497-1500.)

One example of a PNA moiety is N-(2-aminoethyl)-glycine. Further examples of PNA moieties include cyclohexyl PNA, retro-inverso, phosphone, propionyl and aminoproline PNA.

PNA can be chemically synthesized by methods known in the art, e.g. by modified Fmoc or tBoc peptide synthesis protocols. The PNA has many desirable properties, including high melting temperatures (T_m), high base-pairing specificity with nucleic acid and an uncharged

molecular backbone. Additionally, the PNA does not confer RNase H sensitivity on the target RNA, and generally has good metabolic stability.

Peptide nucleic acids are also commercially available from Applied Biosystems (Foster City, California, USA).

In another embodiment, the anti-microRNA molecule comprises at least one morpholino phosphoroamidate nucleotide moiety. A morpholino phosphoroamidate nucleotide moiety is a modified moiety which is nuclease resistant. Such moieties are known in the art. Molecules comprising more than one morpholino phosphoroamidate nucleotide moiety are referred to as morpholino (MF) nucleic acids. See structure 8 in figure 1. Heasman, *Dev. Biol.* **243**, 209-214 (2002). Morpholino oligonucleotides are commercially available from Gene Tools LLC (Corvallis, Oregon, USA).

In another embodiment, the anti-microRNA molecule comprises at least one cyclohexene nucleotide moiety. A cyclohexene nucleotide moiety is a modified moiety which is nuclease resistant. Such moieties are known in the art. Molecules comprising more than one cyclohexene nucleotide moiety are referred to as cyclohexene nucleic acids (CeNA). See structure 10 in figure 1. Wang *et al.*, *J. Am. Chem. Soc.* **122**, 8595-8602 (2000), Verbeure *et al.*, *Nucleic Acids Res.* **29**, 4941-4947 (2001).

In another embodiment, the anti-microRNA molecule comprises at least one tricyclo nucleotide moiety. A tricyclo nucleotide moiety is a modified moiety which is nuclease resistant. Such moieties are known in the art. Steffens *et al.*, *J. Am. Chem. Soc.* **119**, 11548-11549 (1997), Renneberg *et al.*, *J. Am. Chem. Soc.* **124**, 5993-6002 (2002). Molecules comprising more than one tricyclo nucleotide moiety are referred to as tricyclo nucleic acids (tcDNA). See structure 9 in figure 1.

In another embodiment, to increase nuclease resistance of the anti-microRNA molecules of the present invention to exonucleases, inverted nucleotide caps can be attached to the 5' end, the 3' end, or both ends of the molecule. An inverted nucleotide cap refers to a 3'→5' sequence of nucleic acids attached to the anti-microRNA molecule at the 5' and/or the 3' end. There is no limit to the maximum number of nucleotides in the inverted cap just as long as it does not

interfere with binding of the anti-microRNA molecule to its target microRNA. Any nucleotide can be used in the inverted nucleotide cap. Typically, the inverted nucleotide cap is one nucleotide in length. The nucleotide for the inverted cap is generally thymine, but can be any nucleotide such as adenine, guanine, uracil, or cytosine.

Alternatively, an ethylene glycol compound and/or amino linkers can be attached to the either or both ends of the anti-microRNA molecule. Amino linkers can also be used to increase nuclease resistance of the anti-microRNA molecules to endonucleases. The table below lists some examples of amino linkers. The below listed amino linker are commercially available from TriLink Biotechnologies, San Diego, CA.

2'-Deoxycytidine-5-C6 Amino Linker (3' Terminus)
2'-Deoxycytidine-5-C6 Amino Linker (5' or Internal)
3' C3 Amino Linker
3' C6 Amino Linker
3' C7 Amino Linker
5' C12 Amino Linker
5' C3 Amino Linker
5' C6 Amino Linker
C7 Internal Amino Linker
Thymidine-5-C2 Amino Linker (5' or Internal)
Thymidine-5-C6 Amino Linker (3' Terminus)
Thymidine-5-C6 Amino Linker (Internal)

Chimeric anti-microRNA molecules containing a mixture of any of the moieties mentioned above are also known, and may be made by methods known, in the art. See, for example, references cited above, and Wang *et al.*, Proc. Natl. Acad. Sci. USA 96, 13989-13994 (1999), Liang *et al.*, Eur. J. Biochem. 269, 5753-5758 (2002), Lok *et al.*, Biochemistry 41, 3457-3467 (2002), and Damha *et al.*, J. Am. Chem. Soc. 120, 12976-12977 (2002).

The molecules of the invention comprise at least ten contiguous, preferably at least thirteen contiguous, more preferably at least fifteen contiguous, and even more preferably at least twenty contiguous bases that have the same sequence as a sequence of bases in any one of the anti-microRNA molecules shown in Tables 1-4. The anti-microRNA molecules optimally comprise the entire sequence of any one of the anti-microRNA molecule sequences shown in Tables 1-4.

For the contiguous bases mentioned above, up to thirty percent of the base pairs may be substituted by wobble base pairs. As used herein, wobble base pairs refers to either: i) substitution of a cytosine with a uracil, or 2) the substitution of a adenine with a guanine, in the sequence of the anti-microRNA molecule. These wobble base pairs are generally referred to as UG or GU wobbles. Below is a table showing the number of contiguous bases and the maximum number of wobble base pairs in the anti-microRNA molecule:

Table for Number of Wobble Bases

No. of Contiguous Bases	10	11	12	13	14	15	16	17	18
Max. No. of Wobble Base Pairs	3	3	3	3	4	4	4	5	5

No. of Contiguous Bases	19	20	21	22	23
Max. No. of Wobble Base Pairs	5	6	6	6	6

Further, in addition to the addition, deletion, or mismatch at position 11 (see below), up to ten percent, and preferably up to five percent of the contiguous bases can be additions, deletions, mismatches or combinations thereof. Additions refer to the insertion in the contiguous sequence of any moiety described above comprising any one of the bases described above. Deletions refer to the removal of any moiety present in the contiguous sequence. Mismatches refer to the

substitution of one of the moieties comprising a base in the contiguous sequence with any of the above described moieties comprising a different base.

The additions, deletions or mismatches can occur anywhere in the contiguous sequence, for example, at either end of the contiguous sequence or within the contiguous sequence of the anti-microRNA molecule. If the contiguous sequence is relatively short, such as from about ten to about 15 moieties in length, preferably the additions, deletions or mismatches occur at the end of the contiguous sequence. If the contiguous sequence is relatively long, such as a minimum of sixteen contiguous sequences, then the additions, deletions, or mismatches can occur anywhere in the contiguous sequence. Below is a table showing the number of contiguous bases and the maximum number of additions, deletions, mismatches or combinations thereof:

Table for Up to 10%

No. of Contiguous Bases	10	11	12	13	14	15	16	17	18
Max. No. of Additions, Deletions and/or Mismatches	1	1	1	1	1	1	1	1	1

No. of Contiguous Bases	19	20	21	22	23
Max. No. of Additions, Deletions and/or Mismatches	1	2	2	2	2

Table for Up to 5%

No. of Contiguous Bases	10	11	12	13	14	15	16	17	18
Max. No. of Additions, Deletions and/or Mismatches	0	0	0	0	0	0	0	0	0

No. of Contiguous Bases	19	20	21	22	23
Max. No. of Additions, Deletions and/or Mismatches	0	1	1	1	1

Furthermore, no more than fifty percent, and preferably no more than thirty percent, of the contiguous moieties contain deoxyribonucleotide backbone units. Below is a table showing the number of contiguous bases and the maximum number of deoxyribonucleotide backbone units:

Table for Fifty Percent Deoxyribonucleotide Backbone Units

No. of Contiguous Bases	10	11	12	13	14	15	16	17	18
Max. No. of Deoxyribonucleotide Backbone Units	5	5	6	6	7	7	8	8	9

No. of Contiguous Bases	19	20	21	22	23
Max. No. of Deoxyribonucleotide Backbone Units	9	10	10	11	11

Table for Thirty Percent Deoxyribonucleotide Backbone Units

No. of Contiguous Bases	10	11	12	13	14	15	16	17	18
Max. No. of Deoxyribonucleotide Backbone Units	3	3	3	3	4	4	4	5	5

No. of Contiguous Bases	19	20	21	22	23
Max. No. of Deoxyribonucleotide Backbone Units	5	6	6	6	6

It is important that the moiety in the anti-RNA molecule at the position corresponding to position 11 of the microRNA is non-complementary. The moiety in the anti-microRNA molecule corresponding to position 11 of the microRNA can be rendered non-complementary by an addition, deletion or mismatch as described above.

As stated above, the maximum length of the anti-microRNA molecule is 50 moieties. Any number of moieties having any base sequence described above can be added to the contiguous base sequence. The additional moieties can be added to the 5' end, the 3' end, or to both ends of the contiguous sequence.

MicroRNA molecules are derived from genomic loci and are produced from specific microRNA genes. Mature microRNA molecules are processed from precursor transcripts that form local hairpin structures. The hairpin structures are typically cleaved by an enzyme known as Dicer, which generates one microRNA duplex. See Bartel, Cell 116, 281-297 (2004) for a review on microRNA molecules. The article by Bartel is hereby incorporated by reference.

Each strand of a microRNA is packaged in a microRNA ribonucleoprotein complex (microRNP). A microRNP in, for example, humans, also includes the proteins eIF2C2, the helicase Gemin3, and Gemin 4.

The sequence of bases in the anti-microRNA molecules of the present invention can be derived from a microRNA from any species e.g. such as a fly (e.g., *Drosophila melanogaster*), a worm (e.g., *C. elegans*). Preferably the sequence of bases is found in mammals, especially humans (*H. sapiens*), mice (e.g., *M. musculus*), and rats (*R. norvegicus*).

The anti-microRNA molecule is preferably isolated, which means that it is essentially free of other nucleic acids. Essentially free from other nucleic acids means that it is at least 90%, preferably at least 95% and, more preferably, at least 98% free of other nucleic acids.

Preferably, the molecule is essentially pure, which means that the molecule is free not only of other nucleic acids, but also of other materials used in the synthesis of the molecule, such as, for example, enzymes used in the synthesis of the molecule. The molecule is at least 90% free, preferably at least 95% free and, more preferably, at least 98% free of such materials.

The anti-microRNA molecules of the present invention are capable of inhibiting microRNP activity, preferable in a cell. Inhibiting microRNP activity refers to the inhibition of cleavage of the microRNA's target sequence or the repression of translation of the microRNA's target sequence. The method comprises introducing into the cell a single-stranded microRNA molecule.

Any anti-microRNA molecule can be used in the methods of the present invention, as long as the anti-microRNA is complementary, subject to the restrictions described above, to the microRNA present in the microRNP. Such anti-microRNAs include, for example, the anti-microRNA molecules mentioned above (see Table 1-4), and the anti-microRNAs molecules described in international PCT application number WO 03/029459 A2, the sequences of which are incorporated herein by reference.

The invention also includes any one of the microRNA molecules having the sequences as shown in Table 2. The novel microRNA molecules in Table 2 may optionally be modified as described above for anti-microRNA molecules. The other microRNA molecules in Tables 1, 3 and 4 are modified for increased nuclease resistance as described above for anti-microRNA molecules.

Utility

The anti-microRNA molecules and the microRNA molecules of the present invention have numerous *in vivo*, *in vitro*, and *ex vivo* applications.

For example, the anti-microRNA molecules and microRNA of the present invention may be used as a modulator of the expression of genes which are at least partially complementary to the anti-microRNA molecules and microRNA. For example, if a particular microRNA is beneficial for the survival of a cell, an appropriate isolated microRNA of the present invention

may be introduced into the cell to promote survival. Alternatively, if a particular microRNA is harmful (e.g., induces apoptosis, induces cancer, etc.), an appropriate anti-microRNA molecule can be introduced into the cell in order to inhibit the activity of the microRNA and reduce the harm.

In addition, anti-microRNA molecules and/or microRNAs of the present invention can be introduced into a cell to study the function of the microRNA. Any of the anti-microRNA molecules and/or microRNAs listed above can be introduced into a cell for studying their function. For example, a microRNA in a cell can be inhibited with a suitable anti-microRNA molecule. The function of the microRNA can be inferred by observing changes associated with inhibition of the microRNA in the cell in order to inhibit the activity of the microRNA and reduce the harm.

The cell can be any cell which expresses microRNA molecules, including the microRNA molecules listed herein. Alternatively, the cell can be any cell transfected with an expression vector containing the nucleotide sequence of a microRNA.

Examples of cells include, but are not limited to, endothelial cells, epithelial cells, leukocytes (e.g., T cells, B cells, neutrophils, macrophages, eosinophils, basophils, dendritic cells, natural killer cells and monocytes), stem cells, hemopoietic cells, embryonic cells, cancer cells.

The anti-microRNA molecules or microRNAs can be introduced into a cell by any method known to those skilled in the art. Useful delivery systems, include for example, liposomes and charged lipids. Liposomes typically encapsulate oligonucleotide molecules within their aqueous center. Charged lipids generally form lipid- oligonucleotide molecule complexes as a result of opposing charges.

These liposomes-oligonucleotide molecule complexes or lipid- oligonucleotide molecule complexes are usually internalized by endocytosis. The liposomes or charged lipids generally comprise helper lipids which disrupt the endosomal membrane and release the oligonucleotide molecules.

Other methods for introducing an anti-microRNA molecule or a microRNA into a cell include use of delivery vehicles, such as dendrimers, biodegradable polymers, polymers of amino acids, polymers of sugars, and oligonucleotide-binding nanoparticles. In addition, pluoronic gel as a depot reservoir can be used to deliver the anti-microRNA oligonucleotide molecules over a prolonged period. The above methods are described in, for example, Hughes et al., *Drug Discovery Today* 6, 303-315 (2001); Liang et al. *Eur. J. Biochem.* 269 5753-5758 (2002); and Becker et al., In *Antisense Technology in the Central Nervous System* (Leslie, R.A., Hunter, A.J. & Robertson, H.A., eds), pp.147-157, Oxford University Press.

Targeting of an anti-microRNA molecule or a microRNA to a particular cell can be performed by any method known to those skilled in the art. For example, the anti-microRNA molecule or microRNA can be conjugated to an antibody or ligand specifically recognized by receptors on the cell.

The sequences of microRNA and anti-microRNA molecules are shown in Tables 1-4 below. Human sequences are indicated with the prefix “hsa.” Mouse sequences are indicated with the prefix “mmu.” Rat sequences are indicated with the prefix “mo.” *C. elegans* sequences are indicated with the prefix “cel.” Drosophila sequences are indicated with the prefix “dme.”

Table 1: Human, Mouse and Rat microRNA and anti-microRNA sequences.

microRNA name	microRNA sequence (5' to 3')	Anti-microRNA molecule sequence (5' to 3')
hsa-miR-100	AACCCGUAGAUCCGAACUUGUG	CACAAGUUCGGAUCUACGGGUU
hsa-miR-103	AGCAGCAUUGUACAGGGCUAUG	CAUAGCCCUGUACAAUGCUGCU
hsa-miR-105-5p	UCAA AUGCUCAGACUCCUGUGG	CCACAGGAGUCUGAGCAUUUGA
hsa-miR-106a	AAAAGUGCUUACAGUGCAGGUA	UACCUGCACUGUAAGCACUUUU
hsa-miR-106b	UAAAGUGCUGACAGUGCAGUA	UAUCUGCACUGUCAGCACUUUA
hsa-miR-107	AGCAGCAUUGUACAGGGCUAUC	GAUAGCCCUGUACAAUGCUGCU
hsa-miR-10b	UACCCUGUAGAACCGAAUUUGU	ACAAAUUCGGUUCUACAGGGUA
hsa-miR-128b	UCACAGUGAACCGGUCUCUUUC	GAAAGAGACCGGUUCACUGUGA
hsa-miR-130b	CAGUGCAAUGAUGAAAGGGCAU	AUGCCCUUUCAUCAUUGCACUG
hsa-miR-140-3p	UACCACAGGGUAGAACCACGGA	UCCGUGGUUCUACCCUGUGGUA
hsa-miR-142-5p	CCCAUAAAGUAGAAAGCACUAC	GUAGUGCUUUUCUACUUUAUGGG
hsa-miR-151-5p	UCGAGGAGCUCACAGUCUAGUA	UACUAGACUGUGAGCUCCUCGA
hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGG	CCCCUAUCACGAUUAGCAUUAA
hsa-miR-181a	AACAUCUAACGCUGUCGGUGAG	CUCACCGACAGCGUUGAAUGUU
hsa-miR-181b	AACAUCUAUUGCUGUCGGUGGG	CCCACCGACAGCAAUGAAUGUU

microRNA name	microRNA sequence (5' to 3')	Anti-microRNA molecule sequence (5' to 3')
hsa-miR-181c	AACAUUCAACCGUCGGUGAGU	ACUCACCGACAGGUUGAAUGUU
hsa-miR-182	UUUGGCAAUGGUAGAACUCACA	UGUGAGUUCUACCAUUGCCAAA
hsa-miR-183	UAUGGCACUGGUAGAAUUCACU	AGUGAAUUCUACCAGUGCCAU
hsa-miR-184	UGGACGGAGAACUGAUAAAGGGU	ACCCUUAUCAGUUCUCCGUCCA
hsa-miR-185	UGGAGAGAAAGGCAGUUCUGA	UCAGGAACUGCCUUUCUCUCCA
hsa-miR-186	CAAAGAAUUCUCCUUUUGGGCU	AGCCCAAAGGAGAAUUCUUUG
hsa-miR-187	UCGUGUCUUGUGUUGCAGCCGG	CCGGCUGCAACACAAGACACGA
hsa-miR-188-3p	CUCCCAUUGCAGGGUUUGCAG	CUGCAAACCCUGCAUGUGGGAG
hsa-miR-188-5p	CAUCCCUUGCAUGGUGGAGGGU	ACCCUCCACCAUGCAAGGGAUG
hsa-miR-189	GUGCCUACUGAGCUGAUUUCAG	CUGAUUUCAGCUCAGUAGGCAC
hsa-miR-190	UGAUUUGUUUGAUUAUUAAGGU	ACCUAUAUAUCAAACAUAUCA
hsa-miR-191	CAACGGAAUCCCAAAGCAGCU	AGCUGCUUUUGGGAUUCCGUUG
hsa-miR-192	CUGACCUAUGAAUUGACAGCCA	UGGCUGUCAAUUCAUAGGUCAG
hsa-miR-193-3p	AACUGGCCUACAAAGUCCAGU	ACUGGGACUUUGUAGGCCAGUU
hsa-miR-193-5p	UGGGUCUUUGCGGGCAAGAUGA	UCAUCUUGCCCGCAAAGACCCA
hsa-miR-194	UGUAAACAGCAACUCCAUGUGGA	UCCACAUGGAGUUGCUGUUACA
hsa-miR-195	UAGCAGCACAGAAUAUUGGCA	UGCCAAUAUUUCUGUGCUGCUA
hsa-miR-196	UAGGUAGUUUCAUGUUGUUGGG	CCCAACAACAUGAAACUACCUA
hsa-miR-197	UUCACCACCUUCUCCACCCAGC	GCUGGGUGGAGAAGGUGGUGAA
hsa-miR-198	GGUCCAGAGGGGAGAUAGGUUC	GAACCUAUCUCCCCUCUGGACC
hsa-miR-199a-3p	ACAGUAGUCUGCACAUUGGUUA	UAACCAAUGUGCAGACUACUGU
hsa-miR-199a-5p	CCCAGUGUUCAGACUACCUGUU	AACAGGUAGUCUGAACACUGGG
hsa-miR-199b	CCCAGUGUUUAGACUACUGUU	AACAGAUAGUCUAAACACUGGG
hsa-miR-200a	UAACACUGUCUGGUAAACGAUGU	ACAUCGUUACCAGACAGUGUUA
hsa-miR-200b	CUCUAAUACUGCCUGGUAAUGA	UCAUUACCAGGCAGUAUUAGAG
hsa-miR-200c	AAUACUGCCGGGUAAUGAUGGA	UCCAUCAUUACCCGGCAGUAUU
hsa-miR-203	GUGAAAUGUUUAGGACCACUAG	CUAGUGGUCCUAAACAUUUCAC
hsa-miR-204	UUCCCUUUGUCAUCCUUAUGCCU	AGGCAUAGGAUGACAAAGGGAA
hsa-miR-205	UCCUUCAUUCCACCGGAGUCUG	CAGACUCCGGUGGAAUGAAGGA
hsa-miR-206	UGGAAUGUAAGGAAGUGUGUGG	CCACACACUUCUUACAUAUCCA
hsa-miR-208	AUAAGACGAGCAAAAAGCUUGU	ACAAGCUUUUUGCUCGUCUUUAU
hsa-miR-210	CUGUGCGUGUGACAGCGGCUGA	UCAGCCGCGUGACACGCACAG
hsa-miR-211	UUCCCUUUGUCAUCCUUCGCCU	AGGCGAAGGAUGACAAAGGGAA
hsa-miR-212	UAACAGUCUCCAGUCACGGCCA	UGGCCGUGACUGGAGACUGUUA
hsa-miR-213	ACCAUCGACCGUUGAUUGUACC	GGUACAAUCAAACGGUCGAUGGU
hsa-miR-214	ACAGCAGGCACAGACAGGCAGU	ACUGCCUGUCUGUGCCUGCUGU
hsa-miR-215	AUGACCUAUGAAUUGACAGACA	UGUCUGUCAAUUCAUAGGUCAU
hsa-miR-216	UAAUCUCAGCUGGCAACUGUGA	UCACAGUUGCCAGCUGAGAUUA
hsa-miR-217	UACUGCAUCAGGAACUGAUUGG	CCAAUCAGUUCUGAUGCAGUA
hsa-miR-218	UUGUGCUUGAUCUAACCAUGUG	CACAUGGUUAGAUAAGCACAA
hsa-miR-219	UGAUUGUCCAAACGCAAUUCUU	AAGAAUUGCGUUUGGACAAUCA
hsa-miR-220	CCACACCGUAUCUGACACUUUG	CAAAGUGUCAGAUACGGUGUGG
hsa-miR-221	AGCUACAUUGUCUGCUGGGUUU	AAACCCAGCAGACAAUGUAGCU
hsa-miR-222	AGCUACAUCUGGCUACUGGGUC	GACCCAGUAGCCAGAUGUAGCU
hsa-miR-223	UGUCAGUUUGUCAAAUACCCCA	UGGGGUUUUGACAAACUGACA
hsa-miR-224	CAAGUCACUAGUGGUUCCGUUU	AAACGGAACCACUAGUGACUUG
hsa-miR-28-5p	AAGGAGCUCACAGUCUAUUGAG	CUCAAUAGACUGUGAGCUCCUU
hsa-miR-290	CUCAAACUGUGGGGGGCACUUUC	GAAAGUGCCCCCACAGUUUGAG
hsa-miR-296	AGGGCCCCCCCCUCAAUCCUGUU	AACAGGAUUGAGGGGGGGCCCU
hsa-miR-299	UGGUUUACCGUCCCAUAUACA	AUGUAUGUGGGACGGUAAACCA
hsa-miR-301	CAGUGCAAUAGUAUUGUCAAG	CUUUGACAAUACUAUUGCACUG

microRNA name	microRNA sequence (5' to 3')	Anti-microRNA molecule sequence (5' to 3')
hsa-miR-302	UAAGUGCUUCCAUGUUUUGGUG	CACCAAACAUGGAAGCACUUA
hsa-miR-30e	UGUAAACAUCCUUGACUGGAAG	CUUCCAGUCAAGGAUGUUUACA
hsa-miR-320	AAAAGCUGGGUUGAGAGGGCGA	UCGCCCUCUCAACCCAGCUUUU
hsa-miR-321	UAAGCCAGGGAUUGUGGGUUCG	CGAACCCACAAUCCCUGGCUUA
hsa-miR-322	AAACAUGAAUUGCUGCUGUAUC	GAUACAGCAGCAAUUCAUGUUU
hsa-miR-323	GCACAUUACACGGUCCAGCCUCU	AGAGGUCGACCGUGUAAUGUGC
hsa-miR-324-3p	CCACUGCCCCAGGUGCUGCUGG	CCAGCAGCACCUGGGGCAGUGG
hsa-miR-324-5p	CGCAUCCCCUAGGGCAUUGGUG	CACCAAUGCCCUAGGGGAUGCG
hsa-miR-326	CCUCUGGGCCCUCUCCUCCAGCC	GGCUGGAGGAAGGGCCCAGAGG
hsa-miR-328	CUGGCCCUCUCUGCCCUCUCCGU	ACGGAAGGGCAGAGAGGGCCAG
hsa-miR-329	AACACACCCAGCUAACCUCUUUU	AAAAAGGUUAGCUGGGUGUGUU
hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	ACAACCAGCUAAGACACUGCCA
hsa-miR-34b	AGGCAGUGUCAUAGCUGAUUG	CAAUCAGCUAAUGACACUGCCU
hsa-miR-34c	AGGCAGUGUAGUAGCUGAUUG	CAAUCAGCUAACUACACUGCCU
hsa-miR-92	UAUUGCACUUGUCCCGGCCUGU	ACAGGCCGGGACAAGUGCAAUA
hsa-miR-93	AAAGUGCUGUUCGUGCAGGUAG	CUACCUGCACGAACAGCACUUU
hsa-miR-95	UUCAACGGGUAAUUUAUUGAGCA	UGCUCAAUAAAUAACCCGUUGAA
hsa-miR-96	UUUGGCACUAGCACAUUUUUGC	GCAAAAUGUGCUAGUGCCAAA
hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	AACAAUACAACUUAACCUCA
mmu-miR-106a	CAAAGUGCUAACAGUGCAGGUA	UACCUGCACUGUAGCACUUUG
mmu-miR-10b	CCCUGUAGAACCGAUUUUGUGU	ACACAAAUUCGGUUCUACAGGG
mmu-miR-135b	UAUGGCUUUUCAUUCCUAUGUG	CACAUAGGAAUGAAAAGCCAUA
mmu-miR-148b	UCAGUGCAUCACAGAACUUUGU	ACAAAGUUCUGUGAUGCACUGA
mmu-miR-151-3p	CUAGACUGAGGCUCUUGAGGA	UCCUCAAGGAGCCUCAGUCUAG
mmu-miR-155	UUAAUGCUAAUUGUGAUAGGGG	CCCCUAUCACAAUAGCAUUA
mmu-miR-199b	CCCAGUGUUUAGACUACCUGUU	AACAGGUAGUCUAAACACUGGG
mmu-miR-200b	UAAUACUGCCUGGUAUGAUGA	UCAUCAUUAACAGGCAGUAUUA
mmu-miR-203	UGAAAUGUUUAGGACCACUAGA	UCUAGUGGUCCUAAACAUUUC
mmu-miR-211	UUCCCUUUGUCAUCCUUGCCU	AGGCAAAGGAUGACAAAGGGAA
mmu-miR-217	UACUGCAUCAGGAACUGACUGG	CCAGUCAGUUCUGAUGCAGUA
mmu-miR-224	UAAGUCACUAGUGGUUCCGUUU	AAACGGAACCACUAGUGACUUA
mmu-miR-28-3p	CACUAGAUGUGAGCUGCUGGA	UCCAGCAGCUCACAAUCUAGUG
mmu-miR-290	CUCAAACUAUGGGGGCACUUUU	AAAAGUGCCCCCAUAGUUUGAG
mmu-miR-291-3p	AAAGUGCUCUCCAUUUGUGUGC	GCACACAAAGUGGAAGCACUUU
mmu-miR-291-5p	CAUCAAGUGGAGGCCCUCUCU	AGAGAGGGCCUCCAUUUGAUG
mmu-miR-292-3p	AAGUGCCGCCAGGUUUUGAGUG	CACUCAAAACCUGGCGGCACUU
mmu-miR-292-5p	ACUCAAAACUGGGGGCUCUUUUG	CAAAAGAGCCCCAGUUUGAGU
mmu-miR-293	AGUGCCGCAGAGUUUGUAGUGU	ACACUACAAACUCUGCGGCACU
mmu-miR-294	AAAGUGCUCUCCUUUUGUGUGU	ACACACAAAAGGGAAGCACUUU
mmu-miR-295	AAAGUGCUCUACUUUUGAGUC	GACUCAAAAGUAGUAGCACUUU
mmu-miR-297	AUGUAUGUGUGCAUGUGCAUGU	ACAUGCACAUGCACACAUACAU
mmu-miR-298	GGCAGAGGAGGGCUGUUCUUC	GGAAGAACAGCCCUCUCUGCC
mmu-miR-300	UAUGCAAGGGCAAGCUCUCUUC	GAAGAGAGCUUGCCCUUGCAUA
mmu-miR-31	AGGCAAGAUGCUGGCAUAGCUG	CAGCUAUGCCAGCAUCUUGCCU
mmu-miR-322	AAACAUGAAGCGCUGCAACACC	GGUGUUGCAGCGCUUCAUGUUU
mmu-miR-325	CCUAGUAGGUGCUCAGUAAGUG	CACUACUGAGCACCUCUAGG
mmu-miR-326	CCUCUGGGCCCUCUCCUCCAGUC	GACUGGAGGAAGGGCCCAGAGG
mmu-miR-330	GCAAAGCACAGGGCCUGCAGAG	CUCUGCAGGCCCUGUGCUUUGC
mmu-miR-331	GCCCCUGGGCCUAUCCUAGAAC	GUUCUAGGAUAGGCCCAGGGGC
mmu-miR-337	UUCAGCUCCUAUAUGAUGCCUU	AAGGCAUCAUAUAGGAGCUGAA
mmu-miR-338	UCCAGCAUCAGUGAUUUUGUUG	CAACAAAUCACUGAUGCUGGA

microRNA name	microRNA sequence (5' to 3')	Anti-microRNA molecule sequence (5' to 3')
mmu-miR-339	UCCCUGUCCUCCAGGAGCUCAC	GUGAGCUCCUGGAGGACAGGGA
mmu-miR-340	UCCGUCUCAGUUACUUUAUAGC	GCUAUAAAGUAAACUGAGACGGA
mmu-miR-341	UCGAUCGGUCGGUCGGUCAGUC	GACUGACCGACCGACCGAUCCA
mmu-miR-342	UCUCACACAGAAAUCGCACCCG	CGGGUGCGAUUUCUGUGUGAGA
mmu-miR-344	UGAUCUAGCCAAAGCCUGACUG	CAGUCAGGCUUUGGCUAGAUA
mmu-miR-345	UGCUGACCCCUAGUCCAGUGCU	AGCACUGGACUAGGGGUCAGCA
mmu-miR-346	UGUCUGCCCGAGUGCCUGCCUC	GAGGCAGGCACUCGGGCAGACA
mmu-miR-34b	UAGGCAGUGUAAUUAAGCUGAUU	AAUCAGCUAAUUAACACUGCCUA
mmu-miR-350	UUCACAAAGCCCAUACACUUUC	GAAAGUGUAUGGGCUUUGUGAA
mmu-miR-351	UCCCUGAGGAGCCCUUUGAGCC	GGCUCAAAGGGCUCCUCAGGGA
mmu-miR-7b	UGGAAGACUUGUGAUUUUGUUG	CAACAAAUCACAAGUCUUCCA
mmu-miR-92	UAUUGCACUUGUCCCGGCCUGA	UCAGGCCGGGACAAGUGCAAUA
mmu-miR-93	CAAAGUGCUGUUCGUGCAGGUA	UACCUGCACGAACAGCACUUUG
rno-miR-327	CCUUGAGGGGCAUGAGGGUAGU	ACUACCCUCAUGCCCCUCAAGG
rno-miR-333	GUGGUGUGCUAGUUACUUUUGG	CCAAAAGUAAACUAGCACACCAC
rno-miR-335	UCAAGAGCAAUAAACGAAAAUG	CAUUUUUCGUUAUUGCUCUUGA
rno-miR-336	UCACCCUCCAUUAUCUAGUCUC	GAGACUAGAUUAUGGAAGGGUGA
rno-miR-343	UCUCCCUCCGUGUGCCCAGUAU	AUACUGGGCACACGGAGGGAGA
rno-miR-347	UGUCCCUUGGGUCGCCAGCU	AGCUGGGCGACCCAGAGGGACA
rno-miR-349	CAGCCCUGCUGUCUUAACCUCU	AGAGGUUAAGACAGCAGGGCUG
rno-miR-352	AGAGUAGUAGGUUGCAUAGUAC	GUACUAUGCAACCUACUACUCU

Table 2: Novel Human microRNA and anti-microRNA sequences.

microRNA name	microRNA sequence (5' to 3')	Anti-microRNA molecule sequence (5' to 3')
hsa-miR-361	UUAUCAGAAUCUCCAGGGGUAC	GUACCCCUUGGAGAUUCUGAUAA
hsa-miR-362	AAUCCUUGGAACCUAGGUGUGA	UCACACCUAGGUUCCAAGGAUU
hsa-miR-363	AUUGCACGGUAUCCAUCUGUAA	UUACAGAUGGAUACCGUGCAAU
hsa-miR-364	CGGCGGGGACGGCGAUUGGUCC	GGACCAAUCGCCGUCGCCGCCG
hsa-miR-365	UAAUGCCCCUAAAAUCCUUAU	AUAAGGAUUUUUAGGGGCAUUA
hsa-miR-366	UAAUCUGGUUGAACAAACUGAACC	GGUUCAGUUGUUAACCAAGUUA

Table 3: C. elegans microRNA and anti-microRNA sequences.

microRNA name	microRNA sequence (5' to 3')	Anti-microRNA molecule sequence (5' to 3')
Cel-let-7	UGAGGUAGUAGGUUGUAUAGUU	AACUAUACAACCUACUACCUCU
Cel-lin-4	UCCCUGAGACCUCAAGUGUGAG	CUCACACUUGAGGUCUCAGGGA
Cel-miR-1	UGGAAUGUAAAGAAGUAUGUAG	CUACAUACUUCUUUACAUUCCA
Cel-miR-2	UAUCACAGCCAGCUUUGAUGUG	CACAUCAAAGCUGGCUGUGAUA
Cel-miR-34	AGGCAGUGUGGUUAGCUGGUUG	CAACCAGCUAACCACACUGCCU
Cel-miR-35	UCACCGGGUGGAAACUAGCAGU	ACUGCUAGUUUCCACCCGGUGA
Cel-miR-36	UCACCGGGUGAAAAUUCGCAUG	CAUGCGAAUUUUCACCCGGUGA
Cel-miR-37	UCACCGGGUGAACACUUGCAGU	ACUGCAAGUGUUCACCCGGUGA
Cel-miR-38	UCACCGGGGAGAAAAACUGGAGU	ACUCCAGUUUUUCUCCCGGUGA
Cel-miR-39	UCACCGGGUGUAAAUCAGCUUG	CAAGCUGAUUUUACACCCGGUGA

microRNA name	microRNA sequence (5' to 3')	Anti-microRNA molecule sequence (5' to 3')
Cel-miR-40	UCACCGGGUGUACAUCAGCUAA	UUAGCUGAUGUACACCCGGUGA
Cel-miR-41	UCACCGGGUGAAAAUACCCUA	UAGGUGAUUUUUCACCCGGUGA
Cel-miR-42	CACCGGGUUAACAUCUACAGAG	CUCUGUAGAUGUUAACCCGGUG
Cel-miR-43	UAUCACAGUUUACUUGCUGUCG	CGACAGCAAGUAAACUGUGAUA
Cel-miR-44	UGACUAGAGACACAUCAGCUU	AAGCUGAAUGUGUCUCUAGUCA
Cel-miR-45	UGACUAGAGACACAUCAGCUU	AAGCUGAAUGUGUCUCUAGUCA
Cel-miR-46	UGUCAUGGAGUCGCUCUCUUCA	UGAAGAGAGCGACUCCAUGACA
Cel-miR-47	UGUCAUGGAGGCGCUCUCUUCA	UGAAGAGAGCGCCUCCAUGACA
Cel-miR-48	UGAGGUAGGCUCAGUAGAUGCG	CGCAUCUACUGAGCCUACCUCU
Cel-miR-49	AAGCACCACGAGAAGCUGCAGA	UCUGCAGCUUCUCGUGGUGCUU
Cel-miR-50	UGAU AUGUCUGGUUAUUCUUGG	CCCAAGAAUACCAGACAUAUCA
Cel-miR-51	UACCCGUAGCUCCUAUCCAUGU	ACAUGGAUAGGAGCUACGGGUA
Cel-miR-52	CACCCGUACAUAUGUUUCCGUG	CACGGAAACAUAUGUACGGGUG
Cel-miR-53	CACCCGUACAUAUGUUUCCGUG	CACGGAAACAAAUGUACGGGUG
Cel-miR-54	UACCCGUAUUCUUAUAAUCCG	CGGAUUAUGAAGAUUACGGGUA
Cel-miR-55	UACCCGUAUAAGUUUCUGCUGA	UCAGCAGAAACUUAUACGGGUA
Cel-miR-56	UACCCGUAUAUGUUUCCGCUGAG	CUCAGCGGAAACAUAUACGGGUA
Cel-miR-57	UACCCUGUAGAUCGAGCUGUGU	ACACAGCUCGAUCUACAGGGUA
Cel-miR-58	UGAGAU CGUUCAGUACGGCAAU	AUUGCCGUACUGAACGAUCUCA
Cel-miR-59	UCGAAUCGUUUAUCAGGAUGAU	AUCAUCCUGAUAAACGAUUCGA
Cel-miR-60	UAUUAUGCACAUAUUUCUAGUUC	GAACUAGAAAAUGUGCAUAAUA
Cel-miR-61	UGACUAGAACC GUUACUCAUCU	AGAUGAGUAACGGUUCUAGUCA
Cel-miR-62	UGAU AUGUAAUCUAGCUUACAG	CUGUAAGCUAGAUUACAUAUCA
Cel-miR-63	AUGACACUGAAGCGAGUUGGAA	UUCCAACUCGCUUCAGUGUCAU
Cel-miR-64	UAUGACACUGAAGCGUUAACCGA	UCGGUAACGCUUCAGUGUCAUA
Cel-miR-65	UAUGACACUGAAGCGUAACCGA	UCGGUUAACGCUUCAGUGUCAUA
Cel-miR-66	CAUGACACUGAUUAGGGAUGUG	CACAUCCCUAAUCAGUGUCAUG
Cel-miR-67	UCACAACCUCUAGAAAGAGUA	UACUCUUUCUAGGAGGUUGUGA
Cel-miR-68	UCGAAGACUCAAAAGUGUAGAC	GUCUACACUUUUGAGUCUUCGA
Cel-miR-69	UCGAAAAUUA AAAAGUGUAGAA	UUCUACACUUUUUAAUJUUCGA
Cel-miR-70	UAAUACGUCGUUGGUGUUUCCA	UGGAAACACCAACGACGUUAUA
Cel-miR-71	UGAAAGACAUGGGUAGUGAACG	CGUUCACUACCCAUGUCUUUCA
Cel-miR-72	AGGCAAGAUGUUGGCAUAGCUG	CAGCUAUGCCAACAUCUUGCCU
Cel-miR-73	UGGCAAGAUGUAGGCAGUUCAG	CUGAACUGCCUACAUCUUGCCA
Cel-miR-74	UGGCAAGAAAUGGCAGUCUACA	UGUAGACUGCCAUUUCUUGCCA
Cel-miR-75	UUAAGCUACCAACCGGCUUCA	UGAAGCCGGUUGGUAGCUUUA
Cel-miR-76	UUCGUUGUUGAUGAAGCCUUGA	UCAAGGCUUCAUCAACAACGAA
Cel-miR-77	UUCAUCAGGCCAUAGCUGUCCA	UGGACAGCUAUGGCCUGAUGAA
Cel-miR-78	UGGAGGCCUGGUUGUUUGUGCU	AGCACAAACAACCAGGCCUCCA
Cel-miR-79	AUAAAGCUAGGUUACCAAAGCU	AGCUUUGGUAACCUAGCUUUAU
Cel-miR-227	AGCUUUCGACAUGAUUCUGAAC	GUUCAGAAUCAUGUCGAAAGCU
Cel-miR-80	UGAGAUCAUUAUUGAAAGCCG	CGGCUUUAACUAAUGAUCUCA
Cel-miR-81	UGAGAUCAUCGUGAAAGCUAGU	ACUAGCUUUCACGAUGAUCUCA
Cel-miR-82	UGAGAUCAUCGUGAAAGCCAGU	ACUGGCUUUCACGAUGAUCUCA
Cel-miR-83	UAGCACC AUUAUAAUUCAGUAA	UUACUGAAUUUAU AUGGUGCUA
Cel-miR-84	UGAGGUAGUAUGUAAUUAUGUA	UACAAUAUUA CAUACUACCUCU
Cel-miR-85	UACAAAGUAUUUGAAAAGUCGU	ACGACUUUUCAAAUACUUGUA
Cel-miR-86	UAAGUGAAUGCUUUGCCACAGU	ACUGUGGCAAAGCAUUCACUUA
Cel-miR-87	GUGAGCAAAGUUUCAGGUGUGC	GCACACCUGAAACUUUGCUCAC
Cel-miR-90	UGAU AUGUUGUUUGAAUGCCCC	GGGGCAUUCAAACAACAUAUCA
Cel-miR-124	UAAGGCACGCGGUGAAUGCCAC	GUGGCAUUCACCGCGUGCCUUA

microRNA name	microRNA sequence (5' to 3')	Anti-microRNA molecule sequence (5' to 3')
Cel-miR-228	AAUGGCACUGCAUGAAUUCACG	CGUGAAUUCAUGCAGUGCCAUU
Cel-miR-229	AAUGACACUGGUUAUCUUUCC	GGAAAAGAUAAACCAGUGUCAUU
Cel-miR-230	GUAUUAGUUGUGCGACCAGGAG	CUCCUGGUCGCACAACUAAUAC
Cel-miR-231	UAAGCUCGUGAUCAACAGGCAG	CUGCCUGUUGAUCACGAGCUUA
Cel-miR-232	UAAAUGCAUCUUAACUGCGGUG	CACCGCAGUUAAGAUGCAUUUA
Cel-miR-233	UUGAGCAAUGCGCAUGUGCGGG	CCCGCACAUGCGCAUUGCUCAA
Cel-miR-234	UUAUUGCUCGAGAAUACCCUUU	AAAGGGUAUUCUCGAGCAAUAA
Cel-miR-235	UAUUGCACUCUCCCCGGCCUGA	UCAGGCCCGGGGAGAGUGCAAUA
Cel-miR-236	UAAUACUGUCAGGUAAUGACGC	GCGUCAUUACCUGACAGUAUUA
Cel-miR-237	UCCCUGAGAAUUCUCGAACAGC	GCUGUUCGAGAAUUCUCAGGGA
Cel-miR-238	UUUGUACUCCGAUGCCAUUCAG	CUGAAUGGCAUCGGAGUACAAA
Cel-miR-239a	UUUGUACUACACAUAAGGUACUG	CAGUACCUAUGUGUAGUACAAA
Cel-miR-239b	UUUGUACUACACAAAAGUACUG	CAGUACUUUUGUGUAGUACAAA
Cel-miR-240	UACUGGCCCCCCAAAUCUUCGCU	AGCGAAGAUUUGGGGGCCAGUA
Cel-miR-241	UGAGGUAGGUGCGAGAAAUGAC	GUCAUUUCUCGCACCUACCUC
Cel-miR-242	UUGCGUAGGCCUUUGCUUCGAG	CUCGAAGCAAAGGCCUACGCAA
Cel-miR-243	CGGUACGAUCGCGGCGGGGAUUA	AUAUCCCGCCGCGAUCGUACCG
Cel-miR-244	UCUUUGGUUGUACAAAGUGGUA	UACCACUUUGUACAACCAAAGA
Cel-miR-245	AUUGGUCCCCUCCAAGUAGCUC	GAGCUACUUGGAGGGGACCAAU
Cel-miR-246	UUACAUGUUUCGGGUAGGAGCU	AGCUCCUACCCGAAACAUGUAA
Cel-miR-247	UGACUAGAGCCUAUUCUCUUCU	AGAAGAGAAUAGGCUCUAGUCA
Cel-miR-248	UACACGUGCACGGAUAACGCUC	GAGCGUUAUCCGUGCACGUGUA
Cel-miR-249	UCACAGGACUUUUGAGCGUUGC	GCAACGCUCAAAAGUCCUGUGA
Cel-miR-250	UCACAGUCAACUGUUGGCAUGG	CCAUGCCAACAGUUGACUGUGA
Cel-miR-251	UUAAGUAGUGGUGCCGCUCUUA	UAAGAGCGGCACCACUACUUA
Cel-miR-252	UAAGUAGUAGUGCCGCAGGUAA	UUACCUGCGGCACUACUACUUA
Cel-miR-253	CACACCUCACUAAACACUGACCA	UGGUCAGUGUAGUGAGGUGUG
Cel-miR-254	UGCAAUCUUUCGCGACUGUAG	CUACAGUCGCGAAAGAUUUGCA
Cel-miR-256	UGGAAUGCAUAGAAGACUGUAC	GUACAGUCUUCUAUGCAUCCA
Cel-miR-257	GAGUAUCAGGAGUACCCAGUGA	UCACUGGGUACUCCUGAUACUC
Cel-miR-258	GGUUUUGAGAGGAAUCCUUUA	UAAAAGGAUUCUCUCAAAACC
Cel-miR-259	AGUAAAUCUCAUCCUAAUCUGG	CCAGAUUAGGAUGAGAUUUACU
Cel-miR-260	GUGAUGUCGAACUCUUGUAGGA	UCCUACAAGAGUUCGACAUCAC
Cel-miR-261	UAGCUUUUAGUUUUCACGGUG	CACCGUGAAAACUAAAAAGCUA
Cel-miR-262	GUUUCUCGAUGUUUUCUGAUAC	GUUUCAGAAAACUUCGAGAAAC
Cel-miR-264	GGCGGGUGGUUGUUGUUAUGGG	CCCAUAAACAACAACACCCGCC
Cel-miR-265	UGAGGGAGGAAGGGUGGUUUU	AAAUACCACCCUUCUCCCUCA
Cel-miR-266	AGGCAAGACUUUGGCAAAGCUU	AAGCUUUGCCAAAGUCUUGCCU
Cel-miR-267	CCCGUGAAGUGUCUGCUGCAAU	AUUGCAGCAGACACUUCACGGG
Cel-miR-268	GGCAAGAAUUAGAAGCAGUUUG	CAAACUGCUUCUAAUUCUUGCC
Cel-miR-269	GGCAAGACUCUGGCAAAACUUG	CAAGUUUUGCCAGAGUCUUGCC
Cel-miR-270	GGCAUGAUGUAGCAGUGGAGAU	AUCUCCACUGCUACAUCUUGCC
Cel-miR-271	UCGCCGGGUGGGAAAGCAUUCG	CGAUGCUUUCACCCCGGCGA
Cel-miR-272	UGUAGGCAUGGGUGUUUGGAAG	CUUCCAAACACCCAUGCCUACA
Cel-miR-273	UGCCCGUACUGUGUCGGCUGCU	AGCAGCCGACACAGUACGGGCA

Table 4: Drosophila microRNA and anti-microRNA sequences.

microRNA name	microRNA sequence (5' to 3')	Anti-microRNA molecule sequence (5' to 3')
Dme-miR-263a	GUUAAUGGCACUGGAAGAAUUC	GAAUUCUCCAGUGCCAUAUAC
Dme-miR-184	UGGACGGAGAACUGAUAAAGGGC	GCCCUUAUCAGUUCUCCGUCCA
Dme-miR-274	UUUUGUGACCGACACUAACGGG	CCCGUUAGUGUCGGUCACAAAA
Dme-miR-275	UCAGGUACCUGAAGUAGCGCGC	GCGCGCUACUUCAGGUACCUGA
Dme-miR-92a	CAUUGCACUUGUCCCGGCCUAU	AUAGGCCGGGACAAGUGCAAUG
Dme-miR-219	UGAUUGUCCAAACGCAAUUCUU	AAGAAUUGCGUUUGGACAAUCA
Dme-miR-276a	UAGGAACUUCAUACCGUGCUCU	AGAGCACGGUAUGAAGUUCCUA
Dme-miR-277	UAAAUGCACUAUCUGGUACGAC	GUCGUACCAGAUAGUGCAUUA
Dme-miR-278	UCGGUGGGACUUUCGUCCGUUU	AAACGGACGAAAGUCCCACCGA
Dme-miR-133	UUGGUCCCCUUAACCAGCUGU	ACAGCUGGUUGAAGGGGACCAA
Dme-miR-279	UGACUAGAUCACACUCAUUA	UUAAGAGUGUGGAUCUAGUCA
Dme-miR-33	AGGUGCAUUGUAGUCGCAUUGU	ACAAUGCGACUACAAUGCACCU
Dme-miR-280	UGUAUUUACGUUGCAUAUGAAA	UUUCAUAUGCAACGUAAAUA
Dme-miR-281	UGUCAUGGAAUUGCUCUCUUUG	CAAAGAGAGCAAUCCAUGACA
Dme-miR-282	AAUCUAGCCUCUACUAGGCUUU	AAAGCCUAGUAGAGGCUAGAUU
Dme-miR-283	UAAAUUACAGCUGGUAAUUCUG	CAGAAUUAACAGCUGAUAUUA
Dme-miR-284	UGAAGUCAGCAACUUGAUUCCA	UGGAAUCAAGUUGCUGACUUA
Dme-miR-34	UGGCAGUGUGGUUAGCUGGUUG	CAACCAGCUAACCACACUGCCA
Dme-miR-124	UAAGGCACGCGGUGAAUGCCAA	UUGGCAUUCACCGCGUGCCUUA
Dme-miR-79	UAAAGCUAGAUUACCAAAGCAU	AUGCUUUGGUAAUCUAGCUUA
Dme-miR-276b	UAGGAACUUAUACCGUGCUCU	AGAGCACGGUAUUAAGUUCCUA
Dme-miR-210	UUGUGCGUGUGACAGCGGCUAU	AUAGCCGCUGUCACACGCACAA
Dme-miR-285	UAGCACCAUUCGAAAUCAGUGC	GCACUGAUUUCGAAUGGUGCUA
Dme-miR-100	AACCCGUAAAUCCGAACUUGUG	CACAAGUUCGGAUUUACGGGUU
Dme-miR-92b	AAUUGCACUAGUCCCGGCCUGC	GCAGGCCGGGACUAGUGCAAUU
Dme-miR-286	UGACUAGACCGAACACUCGUGC	GCACGAGUGUUCGGUCUAGUCA
Dme-miR-287	UGUGUUGAAAAUCGUUUGCACG	CGUGCAAACGAUUUUCAACACA
Dme-miR-87	UUGAGCAAAAUUUCAGGUGUGU	ACACACCUGAAAUUUUGCUCAA
Dme-miR-263b	CUUGGCACUGGGAGAAUUCACA	UGUGAAUUCUCCAGUGCCAAG
Dme-miR-288	UUUCAUGUCGAUUUCAUUUCAU	AUGAAAUGAAAUCGACAUGAAA
Dme-miR-289	UAAAUUUUAAGUGGAGCCUGC	GCAGGCUCCACUUAUUUAUUUA
Dme-bantam	UGAGAUCAUUUUGAAAGCUGAU	AUCAGCUUUCAAAUGAUCUCA
Dme-miR-303	UUUAGGUUUCACAGGAAACUGG	CCAGUUUCCUGUGAAACCUAAA
Dme-miR-31b	UGGCAAGAUGUCGGAAUAGCUG	CAGCUAUUCCGACAUCUUGCCA
Dme-miR-304	UAAUCUCAAUUUGUAAAUGUGA	UCACAUUUACAAUUGAGAUUA
Dme-miR-305	AUUGUACUUCAUACGGUGCUCU	AGAGCACCUGAUGAAGUACAAU
Dme-miR-9c	UCUUUGGUUUUCUAGCUGUAGA	UCUACAGCUAGAAUACCAAAGA
Dme-miR-306	UCAGGUACUUGAGACUCUCAA	UUGAGAGUCACUAAGUACCUGA
Dme-miR-9b	UCUUUGGUGAUUUUAGCUGUAU	AUACAGCUAAAUCACCAAAGA
Dme-miR-125	UCCUGAGACCCUAACUUGUGA	UCACAAGUUAGGGUCUCAGGGA
Dme-miR-307	UCACAACCUCCUUGAGUGAGCG	CGCUCACUCAAGGAGGUUGUGA
Dme-miR-308	AAUCACAGGAUUAUACUGUGAG	CUCACAGUAUAAUCCUGUGAUU
dme-miR-31a	UGGCAAGAUGUCGGCAUAGCUG	CAGCUAUGCCGACAUCUUGCCA
dme-miR-309	GCACUGGGUAAAGUUUGUCCUA	UAGGACAAACUUUACCCAGUGC
dme-miR-310	UAUUGCACACUUCGCGGCCUUU	AAAGGCCGGGAAGUGUGCAAUA
dme-miR-311	UAUUGCACAUUCACCGGCCUGA	UCAGGCCGGUGAAUGUGCAAUA
dme-miR-312	UAUUGCACUUGAGACGGCCUGA	UCAGGCCGUCUCAAUGUGCAAUA
dme-miR-313	UAUUGCACUUUUCACAGCCCGA	UCGGGCUGUGAAAAGUGCAAUA
dme-miR-314	UAUUCGAGCCAAUAAGUUCGG	CCGAACUUAUUGGCUCGAAUA

microRNA name	microRNA sequence (5' to 3')	Anti-microRNA molecule sequence (5' to 3')
dme-miR-315	UUUUGAUUGUUGCUCAGAAAGC	GCUUUCUGAGCAACAAUCAAAA
dme-miR-316	UGUCUUUUUCCGCUUACUGGCG	CGCCAGUAAGCGGAAAAAGACA
dme-miR-317	UGAACACAGCUGGUGGUUCCA	UGGAUACCACCAGCUGUGUUA
dme-miR-318	UCACUGGGCUUUGUUUAUCUCA	UGAGAUAAACAAAGCCCAGUGA
dme-miR-2c	UAUCACAGCCAGCUUUGAUGGG	CCCAUCAAGCUGGCUGUGAUA
Dme-miR-iab45p	ACGUUAUCUGAAUGUAUCCUGA	UCAGGAUACAUCAGUAUACGU
Dme-miR-iab43p	CGGUUAACCUUCAGUAUACGUA	UACGUUAUCUGAAGGUUAACCG

EXAMPLES

Example 1: Materials and Methods

Oligonucleotide synthesis

MiR-21 were synthesized using 5'-silyl, 2'-ACE phosphoramidites (Dharmacon, Lafayette, CO, USA) on 0.2 μ mol synthesis columns using a modified ABI 394 synthesizer (Foster City, CA, USA) (Scaringe, Methods Enzymol. 317, 3-18 (2001) and Scaringe, Methods 23, 206-217 (2001)). The phosphate methyl group was removed by flushing the column with 2 ml of 0.2 M 2-carbamoyl-2-cyanoethylene-1,1-dithiolate trihydrate in DMF/water (98:2 v/v) for 30 min at room temperature. The reagent was removed and the column rinsed with 10 ml water followed by 10 ml acetonitrile. The oligonucleotide was cleaved and eluted from the solid support by flushing with 1.6 ml of 40% aqueous methylamine over 2 min, collected in a screwcap vial and incubated for 10 min at 55 °C. Subsequently, the base-treated oligonucleotide was dried down in an Eppendorf concentrator to remove methylamine and water. The residue was dissolved in sterile 2'-deprotection buffer (400 μ l of 100 mM acetate-TEMED, pH 3.8, for a 0.2 μ mol scale synthesis) and incubated for 30 minutes at 60 °C to remove the 2' ACE group. The oligoribonucleotide was precipitated from the acetate-TEMED solution by adding 24 μ l 5 M NaCl and 1.2 ml of absolute ethanol.

2'-O-Methyl oligoribonucleotides were synthesized using 5'-DMT, 2'-O-methyl phosphoramidites (Proligo, Hamburg, Germany) on 1 μ mol synthesis columns loaded with 3'-aminomodifier (TFA) C7 Icaa control pore glass support (Chemgenes, MA, USA). The aminolinker was added in order to also use the oligonucleotides for conjugation to amino group

reactive reagents, such as biotin succinimidyl esters. The synthesis products were deprotected for 16 h at 55 °C in 30% aqueous ammonia and then precipitated by the addition of 12 ml absolute 1-butanol. The full-length product was then gel-purified using a denaturing 20% polyacrylamide gel. 2'-Deoxyoligonucleotides were prepared using 0.2 µmol scale synthesis and standard DNA synthesis reagents (Proligo, Hamburg, Germany).

The sequences of the 2'-O-methyl oligoribonucleotides were 5'-GUCAACAUCAGUCUGAUAAGCUAL (L, 3' aminolinker) for 2'-OMe miR-21, and 5'-AAGGCAAGCUGACCCUGAAGUL for EGFP 2'-OMe antisense, 5'-UGAAGUCCCAGUCGAACGGAAL for EGFP 2'-OMe reverse; the sequence of chimeric 2'-OMe/DNA oligonucleotides was 5'-GTCAACATCAGTCTGATAAGCTAGCGL for 2'-deoxy miR-21 (underlined, 2'-OMe residues), and 5'-AAGGCAAGCTGACCCTGAAGTGCGL for EGFP 2'-deoxy antisense.

The miR-21 cleavage substrate was prepared by PCR-based extension of the partially complementary synthetic DNA oligonucleotides 5'-GAACAATTGCTTTTACAGATGCACATATCGAGGTGAACATCACGTACGTCAACATCATCTGATAAGCTATCGGTTGGCAGAAGCTAT and 5'-GGCATAAAGAATTGAAGAGAGTTTTCTACTGCATACGACGATTCTGTGATTTGTATTCAGCCCATATCGTTTCATAGCTTCTGCCAACCGA. The extended dsDNA was then used as template for a new PCR with primers 5'-TAATACGACTCACTATAGAACAATTGCTTTTACAG and 5'-ATTTAGGTGACACTATAGGCATAAAGAATTGAAGA to introduce the T7 and SP6 promoter sequences for in vitro transcription. The PCR product was ligated into pCR2.1-TOPO (Invitrogen). Plasmids isolated from sequence-verified clones were used as templates for PCR to produce sufficient template for run-off in vitro transcription reactions using phage RNA polymerases (Elbashir et al., EMBO 20, 6877-6888 (2001)). ³²P-Cap-labelling was performed as reported (Martinez et al., Cell 110, 563-574 (2002)).

Plasmids

Plasmids pEGFP-S-21 and pEGFP-A-21 were generated by T4 DNA ligation of preannealed oligodeoxynucleotides 5'-GGCCTCAACATCAGTCTGATAAGCTAGGTACCT

and 5'-GGCCAGGTACCTAGCTTATCAGACTGATGTTGA into NotI digested pEGFP-N-1 (Clontech). The plasmid pHcRed-C1 was from Clontech.

HeLa extracts and miR-21 quantification

HeLa cell extracts were prepared as described (Dignam et al., Nucleic Acid Res. 11 1475-1489 (1983)). 5×10^9 cells from HeLa suspension cultures were collected by centrifugation and washed with PBS (pH7.4). The cell pellet (approx. 15 ml) was re-suspended in two times of its volume with 10mM KCl/1.5 mM $MgCl_2$ /0.5 mM dithiothreitol/10mM HEPES-KOH (pH 7.9) and homogenized by douncing. The nuclei were then removed by centrifugation of the cell lysate at 1000 g for 10 min. The supernatant was spun in an ultracentrifuge for 1 h at 10,5000 g to obtain the cytoplasmic S100 extract. The concentration of KCl of the S100 extract was subsequently raised to 100 mM by the addition of 1 M KCl. The extract was then supplemented with 10% glycerol and frozen in liquid nitrogen.

280 μ g of total RNA was isolated from 1 ml of S100 extract using the acidic guanidinium thiocyanate-phenol-chloroform extraction method (Chomczynski et al., Anal. Biochem. 162, 156-159 (1987)). A calibration curve for miR-21 Northern signals was produced by loading increasing amounts (10 to 30000 pg) of synthetically made miR-21 (Lim et al. et al., Genes & Devel. 17, 991-1008 (2003)). Northern blot analysis was performed as described using 30 μ g of total RNA per well (Lagos-Quintana et al., Science 294, 853-858 (2001)).

In vitro miRNA cleavage and inhibition assay

2'-O-Methyl oligoribonucleotides or 2'-deoxyoligonucleotides were pre-incubated with HeLa S100 at 30 °C for 20 min prior to the addition of the cap-labeled miR-21 target RNA. The concentration of the reaction components were 5 nM target RNA, 1 mM ATP, 0.2 mM GTP, 10 U/ml RNasin (Promega) and 50% HeLa S100 extract in a final reaction volume of 25 μ l. The reaction time was 1.5 h at 30 °C. The reaction was stopped by addition of 200 μ l of 300 mM NaCl/25 mM EDTA/20% w/v SDS/200 mM Tris HCl (pH7.5). Subsequently, proteinase K was added to a final concentration of 0.6 mg/ml and the sample was incubated for 15 min at 65 °C. After phenol/chloroform extraction, the RNA was ethanol-precipitated and separated on a 6% denaturing polyacrylamide gel. Radioactivity was detected by phosphorimaging.

Cell culture and transfection

HeLa S3 and HeLa S3/GFP were grown in 5% CO₂ at 37 °C in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (FBS), 100 unit/ml penicillin, and 100 µg/ml streptomycin. One day before transfection, 105 cells were plated in 500 µl DMEM containing 10% FBS per well of a 24-well plate. Plasmid and plasmid/oligonucleotide transfection was carried out with Lipofectamine2000 (Invitrogen). 0.2 µg pEGFP or its derivatives were cotransfected with 0.3 µg pHcRed with or without 10 pmol of 2'-O-methyl oligoribonucleotide or 10 pmol of 2'-deoxyoligonucleotide per well. Fluorescent cell images were recorded on a Zeiss Axiovert 200 inverted fluorescence microscope (Plan-Apochromat 10x/0.45) equipped with Chroma Technology Corp. filter sets 41001 (EGFP) and 41002c (HcRed) and AxioVision 3.1 software.

Example 2: MicroRNA-21 Cleavage of Target RNA

In order to assess the ability of modified oligonucleotides to specifically interfere with miRNA function, we used our previously described mammalian biochemical system developed for assaying RISC activity (Martinez et al., *Cell* 100, 563-574 (2002)). Zamore and colleagues (Hutvagner et al., *Science* 297, 2056-2050 (2002)) showed that crude cytoplasmic cell lysates and eIF2C2 immunoprecipitates prepared from these lysates contain let-7 RNPs that specifically cleave let-7-complementary target RNAs. We previously reported that in HeLa cells, numerous miRNAs are expressed including several let-7 miRNA variants (Lagos-Quintana et al., *Science* 294, 853-858 (2001)).

To assess if other HeLa cell miRNAs are also engaged in RISC like miRNPs we examined the cleavage of a 32P-cap-labelled substrate RNA with a complementary site to the highly expressed miR-21 (Lagos-Quintana et al., *Science* 294, 853-858 (2001); Mourelatos et al., *Genes & Dev.* 16, 720-728 (2002)). Sequence-specific target RNA degradation was readily observed and appeared to be approximately 2- to 5-fold more effective than cleavage of a similar let-7 target RNA (Figure 2A, lane 1, and data not shown). We therefore decided to interfere with miR-21 guided target RNA cleavage.

Example 3: Anti MicroRNA-21 2'-O-methyl Oligoribonucleotide Inhibited MicroRNA-21-Induced Cleavage of Target RNA

A 24-nucleotide 2'-O-methyl oligoribonucleotide that contained a 3' C7 aminolinker and was complementary to the longest form of the miR-21 was synthesized. The aminolinker was introduced in order to enable post-synthetic conjugation of non-nucleotidic residues such as biotin.

Increasing concentrations of anti miR-21 2'-O-methyl oligoribonucleotide and a control 2'-O-methyl oligoribonucleotide cognate to an EGFP sequence were added to the S100 extract 20 min prior to the addition of 32P-cap-labelled substrate. We determined the concentration of miR-21 in the S100 extract by quantitative Northern blotting to be 50 pM (Lim et al., Genes & Devel. 17, 991-1008 (2003)).

The control EGFP oligonucleotide did not interfere with miR-21 cleavage even at the highest applied concentration (Figure 2A, lanes 2-3). In contrast, the activity of miR-21 was completely blocked at a concentration of only 3 nM (Figure 2A, lane 5), and a concentration of 0.3 nM showed a substantial 60%-70% reduction of cleavage activity (Figure 2, lane 6). At a concentration of 0.03 nM, the cleavage activity of miR-21 was not affected when compared to the lysate alone (Figure 2, lane 1, 7).

Antisense 2'-deoxyoligonucleotides (approximately 90% DNA molecules) at concentrations identical to those of 2'-O-methyl oligoribonucleotides, we could not detect blockage of miR-21 induced cleavage (Figure 2A, lanes 8-10). The 2'-deoxynucleotides used in this study were protected against 3'-exonucleases by the addition of three 2'-O-methyl ribonucleotide residues.

Example 4: Anti MicroRNA-21 2'-O-methyl Oligoribonucleotide Inhibited MicroRNA-21-Induced Cleavage of Target RNA *In Vitro*

In order to monitor the activity of miR-21 in HeLa cells, we constructed reporter plasmids that express EGFP mRNA that contains in its 3' UTR a 22-nt sequence complementary to miR-21 (pEGFP-S-21) or in sense orientation to miR-21 (p-EGFP-A-21). Endogenous miRNAs have previously been shown to act like siRNAs by cleaving reporter mRNAs carrying

sequences perfectly complementary to miRNA. To monitor transfection efficiency and specific interference with the EGFP indicator plasmids, the far-red fluorescent protein encoding plasmid pHcRed-C1 was cotransfected.

Expression of EGFP was observed in HeLa cells transfected with pEGFP and pEGFP-A-21 (Figure 3, rows 1 and 2), but not from those transfected with pEGFP-S-21 (Figure 3, row 3). However, expression of EGFP from pEGFP-S-21 was restored upon cotransfection with anti miR-21 2'-O-methyl oligoribonucleotide (Figure 3, row 4). Consistent with our above observation, the 2'-deoxy anti miR-21 oligonucleotide showed no effect (Figure 3, row 5).

Similarly, cotransfection of the EGFP 2'-O-methyl oligoribonucleotide in sense orientation with respect to the EGFP mRNA (or antisense to EGFP guide siRNA) had no effect (Figure 3, row 6).

We have demonstrated that miRNP complexes can be effectively and sequence-specifically inhibited with 2'-O-methyl oligoribonucleotides antisense to the guide strand positioned in the RNA silencing complex.

What we claim is:

1. An isolated single stranded anti-microRNA molecule comprising a minimum of ten moieties and a maximum of fifty moieties on a molecular backbone, the molecular backbone comprising backbone units, each moiety comprising a base bonded to a backbone unit, each base forming a Watson-Crick base pair with a complementary base wherein:

at least ten contiguous bases have the same sequence as a sequence of bases in any one of the anti-microRNA molecules shown in Tables 1-4, except that up to thirty percent of the bases pairs may be wobble base pairs, and up to 10% of the contiguous bases are additions, deletions, mismatches, or combinations thereof;

no more than fifty percent of the contiguous moieties contain deoxyribonucleotide backbone units;

the moiety in the molecule at the position corresponding to position 11 of the microRNA is non-complementary; and

the molecule is capable of inhibiting microRNP activity.

2. A molecule according to claim 1, wherein up to 5% of the contiguous moieties are additions, deletions, mismatches, or combinations thereof.

3. A molecule according to claim 1, wherein at least one of the moieties is a deoxyribonucleotide.

4. A molecule according to claim 3, wherein the deoxyribonucleotide is a modified deoxyribonucleotide moiety.

5. A molecule according to claim 4, wherein the modified deoxyribonucleotide is a phosphorothioate deoxyribonucleotide moiety.

6. A molecule according to claim 4, wherein the modified deoxyribonucleotide is N³-N⁵ phosphoroamidate deoxyribonucleotide moiety.

7. A molecule according to claim 1, wherein at least one of the moieties is a ribonucleotide moiety.
8. A molecule according to claim 7, wherein at least one of the moieties is a modified ribonucleotide moiety.
9. A molecule according to claim 8, wherein the modified ribonucleotide is substituted at the 2' position.
10. A molecule according to claim 9, wherein the substituent at the 2' position is a C₁ to C₄ alkyl group.
11. A molecule according to claim 10, wherein the alkyl group is methyl.
12. A molecule according to claim 10, wherein the alkyl group is allyl.
13. A molecule according to claim 9, wherein the substituent at the 2' position is a C₁ to C₄ alkoxy - C₁ to C₄ alkyl group.
14. A molecule according to claim 13, wherein the C₁ to C₄ alkoxy - C₁ to C₄ alkyl group is methoxyethyl.
15. A molecule according to claim 8, wherein the modified ribonucleotide has a methylene bridge between the 2'-oxygen atom and the 4'-carbon atom.
16. A molecule according to claim 1, wherein at least one of the moieties is a peptide nucleic acid moiety.
17. A molecule according to claim 1, wherein at least one of the moieties is a 2'-fluororibonucleotide moiety.
18. A molecule according to claim 1, wherein at least one of the moieties is a morpholino phosphoroamidate nucleotide moiety.
19. A molecule according to claim 1, wherein at least one of the moieties is a tricyclo nucleotide moiety.

20. A molecule according to claim 1, wherein at least one of the moieties is a cyclohexene nucleotide moiety.
21. A molecule according to claim 1, wherein the molecule comprises at least one modified moiety for increased nuclease resistance.
22. A molecule according to claim 21, wherein the nuclease is an exonuclease.
23. A molecule according to claim 22, wherein the molecule comprises at least one modified moiety at the 5' end.
24. A molecule according to claim 22, wherein the molecule comprises at least two modified moieties at the 5' end.
25. A molecule according to claim 22, wherein the molecule comprises at least one modified moiety at the 3' end.
26. A molecule according to claim 22, wherein the molecule comprises at least two modified moieties at the 3' end.
27. A molecule according to claim 22, wherein the molecule comprises at least one modified moiety at the 5' end and at least one modified moiety at the 3' end.
28. A molecule according to claim 22, wherein the molecule comprises at least two modified moieties at the 5' end and at least two modified moieties at the 3' end.
29. A molecule according to claim 22, wherein the molecule comprises a nucleotide cap at the 5' end, the 3' end or both.
30. A molecule according to claim 22, wherein the molecule comprises an ethylene glycol compound and/or amino linkers at the 5' end, the 3' end, or both.
31. A molecule according to claim 1, wherein the nuclease is an endonuclease.
32. A molecule according to claim 31, wherein the molecule comprises at least one modified moiety between the 5' and 3' end.

33. A molecule according to claim 31, wherein the molecule comprises an ethylene glycol compound and/or amino linker between the 5' end and 3' end.

34. A molecule according to claim 1, wherein all of the moieties are nuclease resistant.

35. A method for inhibiting microRNP activity in a cell, the microRNP comprising a microRNA molecule, the microRNA molecule comprising a sequences of bases complementary of the sequence of bases in a single stranded anti-microRNA molecule, the method comprising introducing into the cell the single-stranded anti-microRNA molecule comprising a sequence of a minimum of ten moieties and a maximum of fifty moieties on a molecular backbone, the molecular backbone comprising backbone units, each moiety comprising a base bonded to a backbone unit, each base forming a Watson-Crick base pair with a complementary base, wherein:

at least ten contiguous bases of the anti-microRNA molecule are complementary to the microRNA, except that up to thirty percent of the bases may be substituted by wobble base pairs, and up to ten percent of the at least ten moieties are addition, deletions, mismatches, or combinations thereof;

no more than fifty percent of the contiguous moieties contain deoxyribonucleotide backbone units; and

the moiety in the molecule at the position corresponding to position 11 of the microRNA is non-complementary.

36. A method according to claim 35, wherein the anti-microRNA is a human anti-microRNA.

37. A method according to claim 35, wherein the anti-microRNA is a mouse anti-microRNA.

38. A method according to claim 35, wherein the anti-microRNA is a rat anti-microRNA.

39. A method according to claim 35, wherein the ant-microRNA is a drosophila microRNA.

40. A method according to claim 35, wherein the anti-microRNA is a C. elegans microRNA.

41. An isolated microRNA molecule comprising a minimum of ten moieties and a maximum of fifty moieties on a molecular backbone, the molecular backbone comprising backbone units, each moiety comprising a base bonded to a backbone unit wherein:

at least ten contiguous bases have the same sequence as a sequence of bases in any one of the microRNA molecules shown in Table 2, except that up to thirty percent of the bases pairs may be wobble base pairs, and up to 10% of the contiguous bases are additions, deletions, mismatches, or combinations thereof; and

no more than fifty percent of the contiguous moieties contain deoxyribonucleotide backbone units.

42. A molecule according to claim 41 having the sequence shown in Table 2.

43. A molecule according to claim 41, wherein the molecule is modified for increased nuclease resistance.

44. A molecule according to claim 41, wherein the moiety at position 11 is an addition, deletion or substitution.

45. An isolated microRNA molecule comprising a minimum of ten moieties and a maximum of fifty moieties on a molecular backbone, the molecular backbone comprising backbone units, each moiety comprising a base bonded to a backbone unit wherein:

at least ten contiguous bases have any one of the microRNA sequences shown in Tables 1, 3 and 4, except that up to thirty percent of the bases pairs may be wobble base pairs, and up to 10% of the contiguous bases are additions, deletions, mismatches, or combinations thereof;

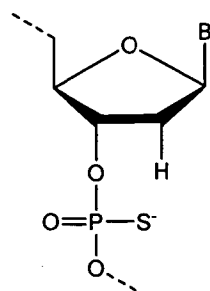
no more than fifty percent of the contiguous moieties contain deoxyribonucleotide backbone units; and

is modified for increased nuclease resistance.

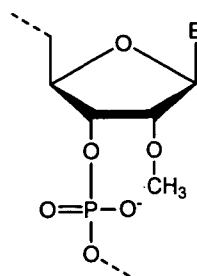
46. A molecule according to claim 45, wherein the molecule is modified for increased nuclease resistance.

47. A molecule according to claim 45, wherein the moiety at position 11 is an addition, deletion, or substitution.

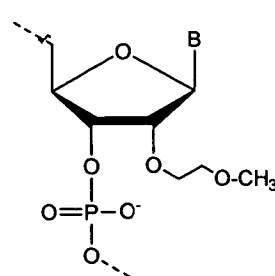
Figure 1



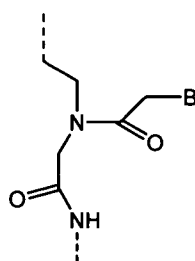
Phosphorothioate DNA Unit
(PS)
Structure 1



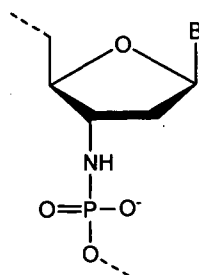
2'-O-methyl RNA unit
(OMe)
Structure 3



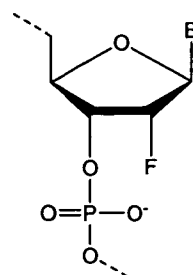
2'-O-methoxy-ethyl RNA unit
(MOE)
Structure 4



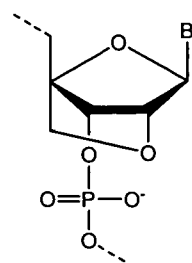
Peptide nucleic acid unit
(PNA)
Structure 6



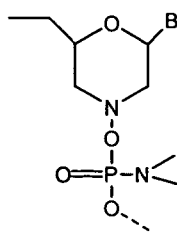
N3'-P5' Phosphoroamidate DNA unit
(NP)
Structure 2



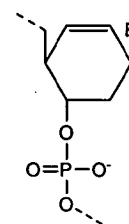
2'-fluoro-ribo nucleic acid unit
(FANA)
Structure 7



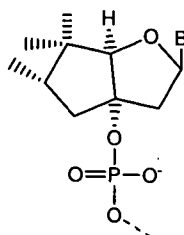
Locked nucleic acid unit
(LNA)
Structure 5



Morpholino phosphoroamidate
nucleic acid unit
(MF)
Structure 8

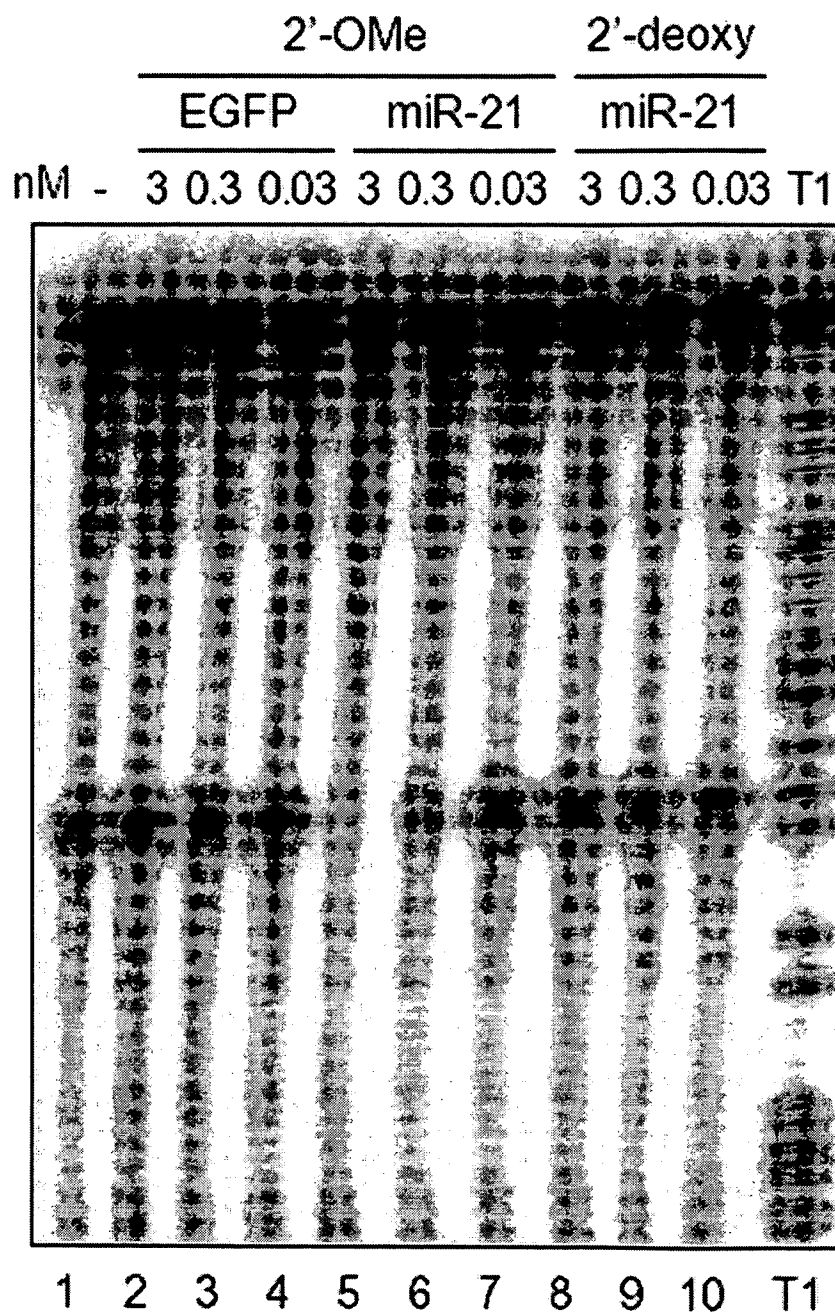


Cyclohexane nucleic acid unit
(CeNA)
Structure 10



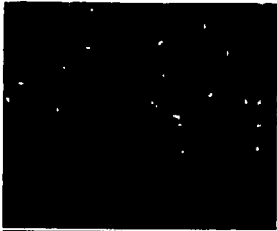


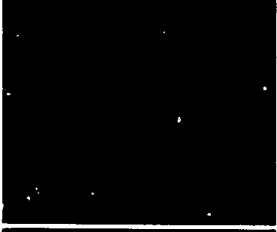

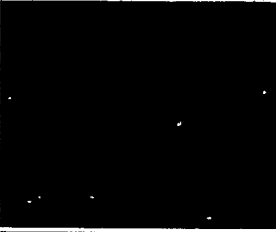

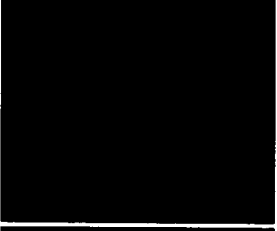

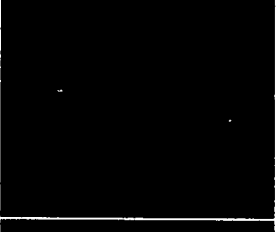
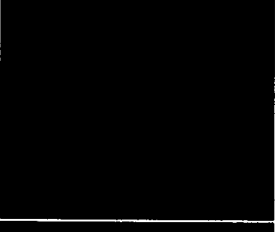
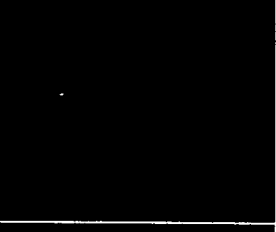
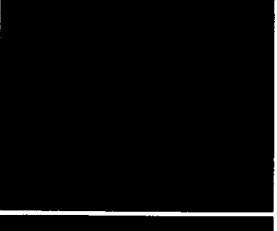
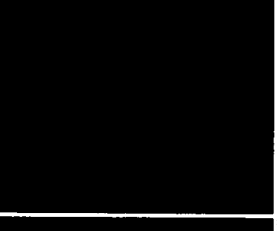

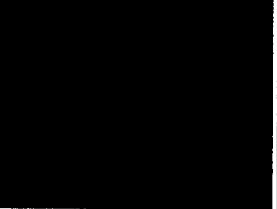
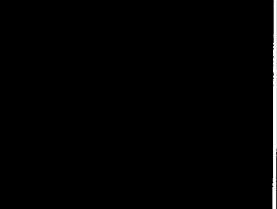
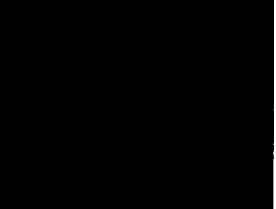
Tricyclonucleic acid unit
Structure 9

Figure 2



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Figure 3

plasmid	oligo	EGFP	HcRed	overlay	
pEGFP					1
pEGFP-A-21					2
pEGFP-S-21					3
	miR-21 2'-OMe				4
	miR-21 2'-deoxy				5
	EGFP 2'-OMe antisense				6

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